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Milk-derived peptides that stimulate Bifidobacterium bifidus

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Claim 2; Page 3; 25pp; German.

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This invention describes milk-derived bifidogenic peptides and their active derivatives or fragments, and combinations of them produced by the central coupling. Such are produced from bovine or human milk by chemical coupling. Such are produced from bovine or human milk by catalying to pH 2 to precipitate proteins. The solution phase is then and cation-exchange HPLC, the fractions adjusted to salt content below conditions. Those fractions adjusted to salt content below conditions. Those fractions for which (BW-BD). (BW-BD) is at least 0.15

XA SHIKER broth containing peptide at 0.2 mg/ml, BD = germ count under similar conditions in a peptide-free control, EW = germ count under similar conditions in a peptide-free control, EW = germ count under similar conditions in a peptide-free control, EW = germ count under similar conditions in a peptide-free control, EW = germ count under similar conditions in a peptide-free control, EW = germ count under similar conditions in a peptide-free control, EW = germ count under similar conditions in a peptide-free control, EW = germ count under similar conditions in a peptide-free control, EW = germ count under similar conditions in a peptide-free control, EW = germ count under similar conditions in a peptide-free control, EW = germ count under similar conditions in a peptide-free control, EW = germ count under similar conditions in a peptide-free control, EW = germ count under similar conditions in a peptide-free control, EW = germ count under similar conditions in a peptide-free control, EW = germ count under similar conditions in a peptide-free control, EW = germ count under similar conditions in a peptide-free control, EW = germ count under similar conditions in a peptide-free control, EW = germ count under similar conditions in a peptide-free control, EW = germ count under similar conditions in a peptide-free control, EW = germ count under similar similar conditions in
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DT 26-JAN-1994 (first entry)

DE Recombinant human kappa casein.

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Nosein; supplement; milk; pharmaceutical; ss.

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Nosys15196-A1.

PD 05-AUG-1993. XX XX EF 25-JAN-1993; 93WO-DK00024. XX PR 23-JAN-1992; 92DK-0000088.

(SYMB-) SYMBICOM AB.

Bergstroem S, Hansson L, Hernell O, Stroemqvist M; Toernell J; WPI; 1993-258675/32.

N-PSDB; AAQ46850

DNA encoding human kappa-casein - used for obtaining recombinant polypeptide(s) for use as nutrient supplements, partic, in infant formulae

Claim 44; Page 88-89; 110pp; English.

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DNA encoding human kappa-casein - used for the prodn. of large amts. of highly purified kappa-casein milk protein for infant use.
                                                                                                                                                                                                                                                                                                                                  means of either a eukaryotic or protective expression system. It is used as a nutrient supplement in milk based products to provide a substantial improvement of the nutritional and biological value of the formulae, making it closer in similarity to human milk. It can also be used as a pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A commercial CDNA library prepd. in lambda gtll from mRNA obtd. from human breast tissue removed during the third trimester of pregnancy was screened with rabbit anti-bovine kappa-fasein CDNA. The CDNA insert of a recombinant phage was amplified by PCR to obtain a full-length clone (AAQ89598) encoding human kappa-casein (AAR72696).
                                                                                                                                                                                                                                                                                                            1 YQRRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 55
                     recombinant human kappa casein is produced in high yields by
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                                                                                                                                                                                                                                         Length 182;
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                                                                                                                                                                                                                              100.0%; Score 305; DB 14;
100.0%; Pred. No. 2.3e-29;
ive 0; Mismatches 0;
                                                                                                                                              on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92US-0962569
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Matches 55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human kappa-casein.
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RESULT 4 AAR92150

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AAR92150 is human milk kappa-casein which is useful as a component of an enteral nutritional product. Kappa-casein has anti-rotaviral activity, it inhibits the attendment of human rotavirus to mammalian cells. The kappa-casein is useful in the treatment and prevention of onset of gastroenteritis and other diarrhoeal diseases caused by rotaviridae esp. in infants, children or immunodeficient patients. Kappa-casein appeared to have no side effects on the subjects treated and is unlikely to be toxic or cause an allergic reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                 Kappa-casein used as anti-rotaviral infection agent in nutritional product - to prevent, retard or treat rotavirus infection, especially in infants, children and immuno-deficient patients
                                                                                                                 Milk protein; kappa-casein; rotavirus inhibition; gastroenteritis; infant formulation; immunodeficiency; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                               Seo AE;
                                                                                       Human milk kappa-casein, inhibits rotaviral infection.
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AAR92150 standard; Protein; 182 AA
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                                                                                                                                                                                                                                                      95WO-US05676.
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94US-0308882.
                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                            Cummings RD,
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                                                                                                                                                                                                                                                                                                                              (ABBO ) ABBOTT LAB.
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                                                       24-0CT-1996
                                                                                                                                                              Homo sapiens
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                            AAR92150
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Gaps 63 YQRRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 117 1 YORRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 55 .; 0 Ouery Match 100.0%; Score 305; DB 17; Length 182; Best Local Similarity 100.0%; Pred. No. 2.3e-29; Matches 55; Conservative 0; Mismatches 0; Indels 0

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AAE18216 standard; Protein; 181 AA AAE18216;

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07-MAY-2002 (first entry)

Human MOL6 protein.

Secreted molecule; MOL6 protein; MOLX; cardiomyopathy; atherosclerosis; diabetes; chromosomal disorder; albinism; anaemia; psoriasis; scarring; liver cirrhosis; neurodegeneration; osteoarthritis; organ rejection; cerebral thrombosis; hypertension; systemic lupus erythematosus; asthma; immune disease; ischaemia; immunodeficiency; rheumatoid arthritis; ulcer; HIY; human immuno deficiency virus; hepatitis; haemostatic disease; pain; haematopoletic; thrombolytic; thrombocytopaenia; Alzheimer's disease; pain; Parkinson's disease; Huntington's disease; muscular disease; stress; ocular disease; growth disorder; depression; epilepsy; contraceptive; 

vulnerary; osteopathic; haemostatic; tranquillser; antidepressant; analgesic; vasotropic; hypotensive; gene therapy. 25..181 /label- Mature\_MOL6\_protein 1..24 /label- Signal\_peptide Location/Qualifiers 2000US-215856P. 2000US-215902P. 2000US-216585P. 2000US-216586P. 2000US-216722P. 2000US-218622P. 2000US-218992P. 2000US-221285P. 03-JUL-2001; 2001WO-US21249 14-FEB-2001; 2001US-268734P WO200206339-A2 Homo sapiens. 07-JUL-2000; 07-JUL-2000; 03-JUL-2000; 03-JUL-2000; 03-JUL-2000; 24-JAN-2002 Key Peptide Protein 

Zerhusen B; Tchernev V, Liu X, Shenoy S, Spytek K, Zerhusen Taupier RJ, Rastelli L, Grosse WM, Szekeres ES; Lepley DM, Shen L, Burgess CE, Shimkets RA; Spaderna SK, Patturajan M, Alsobrook J, Padigaru M;

CURA-) CURAGEN CORP.

WPI; 2002-155038/20. N-PSDB; AAD28950.

Nucleic acids encoding secreted polypeptides, designated MOLX polypeptides, useful for treating a MOLX-associated disorder, e.g. cardiomyopathy, atherosclerosis, diabetes and metabolic disorders

Claim 1; Page 78; 223pp; English.

The particular distributes unitarity and the particular and the particular distributes unitarity and integer from 1 to 8). Sequences of the invention of protein where X is an integer from 1 to 8). Sequences of the invention of are useful for treating or preventing cardiomyopathy, atherosclerosis and disorders related to cell signal processing and theoretical for treating or preventing cardiomyopathy, atherosclerosis and disorders related to cell signal processing and metabolic pathway modulation. The MOLX antibodies are useful for treating or preventing diabetes and disorders related to cell signal processing and metabolic pathway modulation. MOLX sequences are useful for treating or preventing diabetes and disorders, e.g. chromosomal disorders, albinism, anaemia, liver cirrhosis, psoriasis, continuous cardiomy and processing and metabolism, anaemia, liver cirrhosis, psoriasis, carring, neurodegeneration, osteoarthritis, organ rejection, cerebral thromosis, ischaemia, hypertension, systemic lupus erythematosus, immune conferences immunodeficiency, HIV (human immuno deficiency virus), viral, bacterial and fungal infections, hepatitis, rheumatoid arthritis, asthma, chaematopoletic, thrombolytic, haemostatic diseases, thrombocytopaenta, ulcers, Alzhelmer's disease, parkinson's disease, huntington's disease, coular disease, muscular diseases, growth disorders, loss of libido, errore danaection nain and engles are useful for proventing stress, depression, pain and epilepsy. They are useful for preventing chemotherapy side effects and as contraceptives. Sequences of the invention are also useful for gene therapy. The present sequence is human kappa caesin precursor-like protein, MOL6. The patent discloses nucleic acid sequences encoding novel secreted

181 AA; Seguence

Gaps Ĥ DB 23; Length 181; Indels Score 225.5; DB 23; Pred. No. 1.1e-19; 2; Mismatches 7; 73.9%; 81.8%; 45; Conservative Query Match Best Local Similarity Matches 45; Conserv

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This invention describes milk-derived bifidogenic peptides and their active derivatives or fragments, and combinations of them produced by chemical coupling. Such are produced from bovine or human milk by treatment for 2 hr with proteases, then centrifuging to remove fat and acidifying to pH 2 to precipitate proteins. The solution phase is then cation-exchange HPLC, the fractions adjusted to salt content below and cation-exchange HPLC, the fractions adjusted to salt content below growing Bifidobacterium bifidus and Escherichia coll in presence of the fractions. Those fractions for which (Bw-BO) (Ew-EO) is at least 0.15 or selected where Bw = germ count after 16 hr culture of B. bifidus in similar conditions in a peptide-free control, Ew = germ count under hr culture of E. coli in 3 g/l tryptic broth containing peptide at 0.2 mg/ml, EO = germ count under similar conditions in a peptide-free control. The peptides ANW93865-W93888 are used to treat microbe-related control. The peptides ANW93865-W93888 are used to treat microbe-related control. The peptides ANW93865-W93888 are used to treat microbe-related mycoplasma, filaria and plasmodia, e.g. infections, uruses.

CC mycoplasma, filaria and plasmodia, e.g. infections, diarrhoea, colic, and control in carles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YORRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding human kappa-casein - used for obtaining recombinant
polypeptide(s) for use as nutrient supplements, partic. in infant
                     Milk-derived peptides that stimulate Bifidobacterium bifidus
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Pred. No. 5.7e-30;
Mismatches 0;
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Best Local Similarity 100.0%;
Matches 55; Conservative 0,
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N-PSDB; AAQ46850.
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Toernell J;
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Length 55;

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DNA encoding human kappa-casein - used for the prodn. of large amts. of highly purified kappa-casein milk protein for infant use.
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                                means of either a eukaryotic or prokaryotic expression system. It is used as a nutrient supplement in milk based products to provide substantial improvement of the nutritional and biological value of the formulae, making it closer in similarity to human milk. It can
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100.0%; Pred. No. 2.3e-29;
ive 0; Mismatches 0;
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Pred. No. 2.3e-29;
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                                                                                                  used as a pharmaceutical.
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               The recombinant human kappa casein
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nes 55; Conservative
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N-PSDB; AAQ89598.
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1 YORRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF

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Matches

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RESULT 4

Claim 44; Page 88-89; 110pp; English.

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Milk protein; kappa-casein; rotavirus inhibition; gastroenteritis; infant formulation; immunodeficiency; diarrhoea.
                                                                                                                                                                                                                                                Kappa-casein used as anti-rotaviral infection agent in nutritional
                                                                                                                                                                                                                                                         product - to prevent, retard or treat rotavirus infection, especially in infants, children and immuno-deficient patients
                                                                                                                                                                                                                   Seo AE;
                                                   Human milk kappa-casein, inhibits rotaviral infection
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AAR92150 standard; Protein; 182 AA.
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                                                                                                                                                                                                                Cummings
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16-SEP-1994;
                                                                                                               WO9608269-A1
                                    24-OCT-1996
                                                                                                                                 21-MAR-1996.
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AAR92150 is human milk kappa-casein which is useful as a component of an enteral nutritional product. Kappa-casein has anti-rotaviral activity, it inhibits the attachment of human rotavirus to mammalian cells. The kappa-casein is useful in the treatment and prevention of noset of gastroenteritis and other diarrhoeal diseases caused by rotaviridae esp. in infants, children or immunodeficient patients. Kappa-casein appeared to have no side effects on the subjects treated and is unlikely to be toxic or cause an allergic reaction.

182 AA; Sequence

ó ch 100.0%; Score 305; DB 17; Length 182; I Similarity 100.0%; Pred. No. 2.3e-29; 55; Conservative 0; Mismatches 0; Indels 0 est Local Similarity tches 55; Conserv Query Match

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1 YORRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 55

AAE18216 standard; Protein; 181 AA

AAE18216;

07-MAY-2002 (first entry)

Human MOL6 protein.

Secreted molecule; MOL6 protein; MOLX; cardiomyopathy; atherosclerosis; diabetes: chromosomal disorder; albinism; anaemia; psoriasis; scarring; liver cirrhosis; neurodegeneration; osteoarthritis; organ rejection; cerebral thrombosis; hypertension; systemic lupus erythematosus; asthma; himmune disease; ischaemia; immunodeficiency; rheumatoid arthritis; ulcer; HIV; human immuno deficiency virus; hepatitis; haemostatic disease; pain; haematopoietic; thrombolytic; thrombocytopaenia; Alzheimer's disease; Parkinson's disease; Huntington's disease; muscular disease; stress; ocular disease; growth disorder; depression; epilepsy; contraceptive; 

vulnerary; osteopathic; haemostatic; tranquiliser; antidepressant; analgesic; vasotropic; hypotensive; gene therapy. 25..181 /label- Mature\_MOL6\_protein 1..24 /label- Signal\_peptide Location/Qualifiers 2000US-215854P. 2000US-215856P. 2000US-215902P. 2000US-216722P. 2000US-218622P. 2000US-218992P. 2000US-221285P. 2001US-268734P. 03-JUL-2001; 2001WO-US21249. 2000US-216585P 2000US-216586P WO200206339-A2 Homo sapiens 14-FEB:2001; 07-JUL-2000; 07-JUL-2000; .7-JUL-2000; 03-JUL-2000; 24-JAN-2002 Peptide Protein 

(CURA-) CURAGEN CORP.

'n Szekeres ES Shenoy S, Spyc. Tchernev V, Liu X, C., Grosse Taupier RJ, Rastelli L, Grosse Jav DM, Shen L, Burgess CE, Patturajan M, Alsobrook J, I Padigaru M; Spaderna SK,

WPI; 2002-155038/20. N-PSDB; AAD28950.

Nucleic acids encoding secreted polypeptides, designated MOLX polypeptides, useful for treating a MOLX-associated disorder, e.g. cardiomyopathy, atherosclerosis, diabetes and metabolic disorders

Claim 1; Page 78; 223pp; English

molecule (MOL) polypeptides, designated MOLX polypeptides (i.e. a MOL protein where X is an integer from 1 to 8). Sequences of the invention of protein where X is an integer from 1 to 8). Sequences of the invention of are useful for treating or preventing a MOLX-associated disorder in humans. They are useful for treating or preventing action or preventing and molation. The MOLX antibodies are useful for treating or preventing disorders related to cell signal processing and metabolic pathway modulation. MOLX sequences are useful for treating or preventing disorders and disorders related to cell signal processing and metabolic pathway modulation. MOLX sequences are useful for the treatment or diagnosis of other MOLX-associated disorders, e.g. for the treatment or diagnosis of other MOLX-associated disorders, e.g. scarring, neurodegeneration, osteoarthritis, organ rejection, cerebral thrombosis, ischaemia, hypertension, systemic lupus erythematosus, immune diseases, immunodeficiency, HIV (human immuno deficiency virus), viral, hometonic dingal infections, hepatitis, rheumatoid arthritis, asthma, hometonic diseases. haematopoletic, thrombolytic, haemostatic diseases, thrombocytopaenia, ulcers, Alzheimer's disease, Parkinson's disease, Huntington's disease, ocular disease, growth disorders, loss of libido, stress, depression, pain and epilepsy. They are useful for preventing chemotherapy side effects and as contraceptives. Sequences of the invention are also useful for gene therapy. The present sequence The patent discloses nucleic acid sequences encoding novel secreted human kappa caesin precursor-like protein, MoL6

181 AA; Sequence

Gaps ä Length 181; Indels DB 23; 73.9%; Score 225.5; DB 23; 81.8%; Pred. No. 1.1e-19; Live 2; Mismatches 7; Local Similarity 81.8 ses 45; Conservative Query Match Matches

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Human MOL6 protein
Peptide #4550 enco
Peptide #4643 enco
Protein #4449 enco
Human brain expres
                                                                                                           August 11, 2003, 08:16:37; Search time 40.0485 Seconds (without alignments) 217.984 Million cell updates/sec
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Human milk kappa-c
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1 YORRPAIAINNPYVPRIYYA......XLPNSHPPTVVRRPNLHPSF
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/SIDS1/gcgdata/geneseq/geneseqp-embl/Aa1983.DAT;*
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/SIDS1/gcgdata/geneseq/geneseqp-embl/Aa1985.DAT;*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                    OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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AAR72696
AAR92150
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ABB31899
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Human bone marrow Peptide #453 enco Peptide #453 enco Peptide #451 enco Peptide #461 enco Novel human diagno Human Nov93 a prote Bloadhesive precur Sequence of a bioa Human polypeptide Drosophila melanog Spinocerebellar at Human SCA2 polypep Spinocerebellar at Human CA3 protein Human CA4 protein Novel Human Cail Cycle a Antho acid sequenc Propionibacterium Sequence of a bioa Drosophila melanog Japanese sea musse Novel human diagno Brosophila melanog Human mycozadin 3 Human cardiac-spec Bioadhesive precur Sequence of a bioa Drosophila melanog Human cardiac-spec Bioadhesive precur Sequence of a bioa Bioadhesive precur Sequence of a bioa Drosophila melanog Bioadhesive precur Sequence of a bioa	Incord out of the control of the con
193 22 AAM/10275 193 22 AAM/18102 193 22 AAM/18102 193 22 AAM/18102 193 22 AAM/18102 194 22 ABG/3918 904 22 ABG/3918 904 22 ABG/698 134 9 AAP(1827) 134 9 AAP(1827) 1312 24 ABB/187 1312 24 ABB/187 1312 24 ABB/187 1313 19 AAW/1800 1312 24 ABB/187 1313 19 AAW/1800 1313 24 ABB/187 12 ABW/187 13 20 AAP(1827) 13 20 AAP(1827) 14 22 ABB/187 15 21 AAW/187 16 9 AAP(1827) 17 AAW/187 18 9 AAP(1827) 18 12 ABB(1827)	ALIGNMENTS
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711.7 711.5 71	
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#### Bifidobacterium bifidus stimulating peptide 17. AAW93881 standard; peptide; 55 AA. 25-JUN-1999 (first entry) AAW93881; RESULT 1 AAW93881

Bifidogenic peptide; protease; treatment; microbe-related disease; bacteria; fungl; yeast; protozoa; virus; mycoplasma; filaria; plasmodia; infection; inflammation; microbial induced tumour; degenerative disorder; vaginal microflora; antestinal microflora; caries; Bifidobacterium bifidus. WO9914231-A2. 

98DE-1005385. 97DE-1040604. 98WO-EP05899 (FORS/) FORSSMANN W. 16-SEP-1998; 11-FEB-1998; 16-SEP-1997; 25-MAR-1999.

Forssmann W, Liepke C, Zucht H;

WPI; 1999-244022/20.

is produced in high yields by

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Gaps

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Indels

Length 182;

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DNA encoding human kappa-casein – used for obtaining recombinant polypeptide(s) for use as nutrient supplements, partic. In infant
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                                                                                                                                                                                                                                                                                                                                                                                                         Claim 44; Page 88-89; 110pp; English
                                                                                                                                                                                                                                                          Recombinant human kappa casein.
                                                                                                                                                                                                                                                                                                                                                  Hansson
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                                                                                                                                                                                                                                                                                                                                      (SYMB-) SYMBICOM AB
                                                                                                                                                            Best_Local Similarity
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                                                                                                                                            55 AA;
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26-JAN-1994
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means of either a eukaryotic or prokaryotic expression system. It is used as a nutrient supplement in milk based products to provide substantial improvement of the nutritional and biological value of the formulae, making it closer in similarity to human milk. It can
                                                                                                                                                                                                                                                                                                                    100.0%; Score 305; DB 14;
100.0%; Pred. No. 2.3e-29;
ive 0; Mismatches 0;
                                                                                                                                                               also be used as a pharmaceutical. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ham RG, Jeffers KF, Menon RS;
                      The recombinant human kappa casein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR72696 standard; Protein; 182
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                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-160470/21.
N-PSDB; AAQ89598.
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                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                        This invention describes milk-derived bifidogenic peptides and their active derivatives or fragments, and combinations of them produced by active derivatives or fragments, and combinations of them produced by chemical coupling. Such are produced from bovine or human milk by treatment for 2 hr with proteases, then centrifuging to remove fat and caidifying to pH 2 to precipitate proteins. The solution phase is then subjected to reverse-phase high-performance liquid chromatography (HPLC) and cation-exchange HPLC, the fractions adjusted to salt content below cardion-exchange HPLC, the fractions adjusted to salt content below growing Bifidobacterium bifidus and Escherichia coll in presence of the fractions. Those fractions for which (Bw-BO). (Ew-BO) is at least 0.15 are selected where Bw = germ count after 16 hr culture of B. bifidus in a selected where Bw = germ count after 16 hr culture of B. bifidus in 3/1 tryptic broth containing peptide at 0.2 mg/ml. EO = germ count under similar conditions in a peptide-free control. The peptides Anw93865-W93888 are used to treat microbe-related diseases caused by bacteria, fundi, yeast, protozoa, viruses.

Control. The peptides Anw93865-W93888 are used to treat microbe-related diseases caused by bacteria, fundi, yeast, protozoa, viruses.

Control. The peptides thangolds, e.g. infections, inflammation, microblally induced tumours or degenerative disorders, diarrhoea, colic, abnormalities in oral, intestinal or vaginal microflora, or caries.
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                                   Milk-derived peptides that stimulate Bifidobacterium bifidus
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                                                                                                     Page 3; 25pp; German
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DNA encoding human kappa-casein – used for the prodn. of large amts. of highly purified kappa-casein milk protein for infant use.
                                                                                                                               A commercial cDNA library prepd. In lambda gtll from mRNA obtd. from human breast tissue removed during the third trimester of pregnancy was screened with rabbit anti-bovine kappa-casein cDNA. The CDNA insert of a recombinant phage was amplified by PCR to obtain a full-length clone (AAQ89598) encoding human kappa-casein (AAR72696).
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 YQRRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YQRRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF
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                                                                                                                                                                                                                                                                                                                                             100.0%; Score 305; DB 16;
100.0%; Pred. No. 2.3e-29;
iive 0; Mismatches 0;
                                                                                      Disclosure; Column 13-16; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         55; Conservative
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                       182 AA;
                                                                                                                                                                                                                                                                                                          Sequence
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Stroemgvist M;

Hernell O,

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RESULT 4

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NAMES OF COLORS 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR92150 is human milk kappa-casein which is useful as a component of an enteral nutritional product. Kappa-casein has anti-rotaviral activity, it inhibits the attachment of human rotavirus to mammalian cells. The Kappa-casein is useful in the treatment and prevention of onset of gastroenteritis and other diarrhoeal diseases caused by rotaviridee esp. In infants, children or immunodeficient patients. Kappa-casein appeared to have no side effects on the subjects treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YQRRPALAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kappa-casein used as anti-rotaviral infection agent in nutritional product - to prevent, retard or treat rotavirus infection, especially in infants, children and immuno-deficient patients
                                                                                                                                                                   Milk protein; kappa-casein; rotavirus inhibition; gastroenteritis;
infant formulation; immunodeficiency; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is unlikely to be toxic or cause an allergic reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seo AE;
                                                                                                                     Human milk kappa-casein, inhibits rotaviral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 305; DB 17;
Pred. No. 2.3e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mukerji P, Prieto PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 305; Di
llarity 100.0%; Pred. No. 2.33
Conservative 0; Mismatches
AAR92150 standard; Protein; 182 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE18216 standard; Protein; 181 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 9; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                            95WO-US05676.
                                                                                                                                                                                                                                                                                                                                                                                                 94US-0308883
94US-0308882
                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cummings RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-179724/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human MOL6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 AA;
                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                     WO9608269-A1
                                                                                                                                                                                                                                                                                                                                                     05-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                               16-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                      16-SEP-1994;
                                                                                  24-OCT-1996
                                                                                                                                                                                                                                                                                                              21-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baxter JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
                                         AAR92150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE18216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
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The patent discloses nucleic acid sequences encoding novel secreted molecule (MOL) polypeptides, designated MOLX polypeptides (i.e. a MOL protein where X is an integer from 1 to 8). Sequences of the invention are useful for treating or preventing a MOLX-associated disorder in humans. They are useful for treating or preventing cardiomyopathy, atherosclerosis and disorders related to cell signal processing and therosclerosis and disorders related to cell signal processing and metabolic pathway modulation. The MOLX antibodies are useful for treating or preventing diabetes and disorders related to cell signal processing and metabolic pathway modulation. MOLX sequences are useful for treating or preventing diabetes and disorders related to cell signal corressing and metabolic pathway modulation. MOLX sequences are useful for the treatment or diagnosis of other MOLX-associated disorders, e.g. carring, neurodegeneration, osteoarthritis, organ rejection, cerebral thromosomal disorders, albinism, anaemia, liver cirrhosis, psoriasis, contromosomal siscensis, hypertension, systemic lupus erythematosus, immune diseases, immunodeficiency, thymman immuno deficiency virial, bacterial and fungal infections, hepatitis, rheumatoid arthritis, asthma, conternal and fungal infections, hepatitis, rheumatoid arthritis, asthma, culcers, Alzheimer's disease, parkinson's disease, thrombocytopaenia, conternal and fungal infections, barkinson's disease, humanal and conternal and fungal infections, alsease, minorals, alsease, and and alsease, and alsease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocular disease, muscular diseases, growth disorders, loss of libido, stress, depression, pain and epilepsy. They are useful for preventing chemotherapy side effects and as contraceptives. Sequences of the invention are also useful for gene therapy. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
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vulnerary; osteopathic; haemostatic; tranquiliser; antidepressant; analgesic; vasotropic; hypotensive; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding secreted polypeptides, designated MOLX polypeptides, useful for treating a MOLX-associated disorder, e.g. cardiomyopathy, atheroscierosis, diabetes and metabolic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu X, Shenoy S, Spytek K, Zerhusen
, Rastelli L, Grosse WM, Szekeres ES;
Shen L, Burgess CE, Shimkets RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.9%; Score 225.5; DB 23; Length 181; 81.8%; Pred. No. 1.1e-19; tive 2; Mismatches 7; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is human kappa caesin precursor-like protein, MOL6
                                                                                                                                                                                                                                                                                                                                                                   25..181 ' - . . //label= Mature_MOL6_protein
                                                                                                                                                                                                                                                                                       l..24
/label= Signal_peptide
                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tchernev V, Liu X,
Taupier RJ, Rastel
Lepley DM, Shen L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 78; 223pp; English.
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2000US-218992P.
2000US-221285P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUL-2001; 2001WO-US21249
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Best Local Similarity 81.8
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CURA-) CURAGEN CORP.
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N-PSDB; AAD28950.
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Patturajan M,
Alsobrook J, 1
                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Padigaru M;
                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                       Protein
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foctal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                    Human; foetal liver; gene expression; single exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver .
                                                                                                                                                                                                                                                                                    Peptide #4643 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID NO 29772; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 PAIAINNPYVPRTYYANPAVVRP-HAQIPQRQYLPNSHPPTVVRRPNLHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥.
                                                                                                                                              ABB37137 standard; Peptide; 193 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.4%;
ilarity 36.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
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20000S-0608408.
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tes 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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03-AUG-2000;
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26-MAY-2000;
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Matches
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                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                       Peptide #4550 encoded by breast cell single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for measuring gene expression in sample derived from human, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New spatially-addressable set of single exon nucleic acid probes,
            YQRRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF
                                                                                                                                                                                                                                                                                                                                                                      microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     claim 27; SEQ ID NO 14867; 327pp + sequence listing; English.
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Pred. No. 0.76;
4; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank
                                                                                                                                                                            ABB31899 standard; Peptide; 193 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
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20000S-0608408.
20000S-0632366.
20000S-0234687.
20000S-0236359.
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                                                                                                                                                                                                                                                                          (first entry)
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Best Local Similarity 36.0°
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-496933/54.
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                                                                                                                                                                                                                                                                                                                                                                                               disease; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40200157271-A2
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21-SEP-2000;
27-SEP-2000;
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04-OCT-2000;

Penn SG,

breast, useful

26-MAY-2000; 30-JUN-2000;

Homo saptens

09-AUG-2001

01-FEB-2002

RESULT

ò 8 5;

Gaps

3; 53

Indels

23; 22;

Length 193;

Protein #4449 encoded by probe for measuring heart cell gene expression.

53

PAIAINNPYVPRTYYANPAVVRP-HAQIPQRQYLPNSHPPTVVRRPNLHP

Sequence

Best Loc Matches

ô

probe

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probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimmer's disease, multiple sclerosis, schizophrenia, the probes of the invention.
                                                                                                                                                                                                                                                                                                                     Single exon nucleic acid probes for analyzing gene expression in human brains
                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human bone marrow expressed probe encoded protein SEQ ID NO: 30581.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO: 29962; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 PAIAINNPYVPRTYYANPAVVRP-HAQIPQRQYLPNSHPPTVVRRPNLHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 71.5; DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.76;
4; Mismatches
                                                                                                                                                                                                                                                         Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM70275 standard; Protein; 193 AA
                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                      Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC
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                                               30-JAN-2001; 2001WO-US00667
                                                                                                   2000US-0207456
2000US-0608408
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                                                                                                                               2000US-0632366
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2000GB-0024263
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Best Local Similarity 36.0
Matches 18; Conservative
                                                                                                                                                                                                                                                      Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 AA;
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                                                                                               26-MAY-2000;
30-JUN-2000;
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27-SEP-2000;
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                                                                                 04-FEB-2000;
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               09-AUG-2001
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03-AUG-2000;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see MARA1535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, human heart and vascular system e.g. cardiovascular diseases of the human heart and vascular system e.g. cardiovascular disease. hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human brain expressed single exon probe encoded protein SEQ ID NO: 29962.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n expressed exon; gene expression analysis; probe; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAPAHHHP----EYQGQPVVSHPHHIMPPQQHYAPPPPPPPISHPMPP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 193;
        Human; gene expression; heart; microarray; vascular system;
cardlovascular disease; hypertension; cardiac arrhythmia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 71.5; DB 22;
Pred. No. 0.76;
4; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 15; SEQ ID No 24220; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM57857 standard; Protein; 193 AA
                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC.
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36.0%;
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                                                                                                                                                                        30-JAN-2001; 2001WO-US00666
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2000US-0236359
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                        cardiovascular disease; h
congenital heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    microarray; Alzh
epilepsy; cancer
                                                                                                      WO200157274-A2.
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27-SEP-2000;
04-OCT-2000;
                                                                          Homo sapiens
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Penn SG,

AAM57857;

RESULT 9 AAM57857

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Seguence Query Match Best Loc Matches

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Gaps

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23; Indels

the probes are therefore the cervix, notably

9

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Gaps

5; 53

Length 193;

22; 23;

Score 71.5; DB Pred. No. 0.76;

4; Mismatches

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cerrical cancer.
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                               PAPAHHHP----EYQGQPVVSHPHHIMPPQQHYAPPPPPPPPFSHPMPHP 60
                                                                                                                                               5 PAIAINNPYVPRTYYANPAVVRP-HAQIPQRQYLPNSHPPTVVRRPNLHP
epithelial cells. By measuring gene expression, useful in grading and/or staging of diseases of
                                                       at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                   23.4%;
36.0%;
                                                                                                    Query Match 23.4%
Best Local Similarity 36.0%
Matches 18; Conservative
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                                                                               193 AA;
                                                                                                                                                                                                                                                                                                                                    genetic disorder
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03-AUG-2000;
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26-MAY-2000;
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04-OCT-2000;
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                                                                                                                                                                                                                                                    AAM30614;
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                                                                                Sequence
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                                                                                                                 The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #4536 encoded by probe for measuring cervical gene expression
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                           single exon nucleic acid probes useful for
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O
                                                                                            SEQ ID NO: 30581; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                               53
                                                                                                                                                                                                                   Length 193;
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                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                   Score 71.5; DB 22;
Pred. No. 0.76;
1; Mismatches 23;
                                                                         analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID No 22928; 487pp; English
              DR;
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              Rank
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              Chen W,
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36.0%;
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2000US-0608408.
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2000US-0236359
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                                                           qenome-derived
              DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488901/53
                                     WPI; 2001-488900/53
                                                                                                                                                                                                193 AA;
              Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                     cervical cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157278-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2000;
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30-JUN-2000,
                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-2001
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                                                                                             Example 4;
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                                                                                                                                                                                                                                                                                         15
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                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                      Query Match
              SG,
                                                           Human
               Penn
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ID AAM
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                                                                                                                                      Peptide #4651 encoded by probe for measuring placental gene expression.
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                                                                                                                                                                                    microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.4%; Scor.
36.0%; Pred. No. v...
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AAM30614 standard; Protein; 193
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2000US-0608408.
2000US-0632366.
2000US-0234687.
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2000GB-0024263.
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                                                                                                (first entry)
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Matches 18; Conservative
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Human peptide encoded by genome-derived single exon probe SEQ ID 29583.

(first entry)

19-AUG-2002

chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak Syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dyspiasia; pulmonary ciliary dyskinesis; pulmonary hypertension;

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The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in nucleic acid expressed in the human breast. The probes at high stringency to a predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative
                                                                                                                                                                                                      Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      breast disease and non-carcinoma tumours.

Once: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel single exon nucleic acid probe used to measuring gene expression in a human breast {}^{\scriptscriptstyle -}
                                                                                                                                                                        Peptide #4419 encoded by probe for measuring breast gene expression
РАРАННИР----ЕҮДСДРVVSHPHHIMPPQQHYAPPPPPPPPISHPMPHP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID No 14477; 322pp; English.
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                                                                          AAM05737 standard; Protein; 193 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC.
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2000US-0608408
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2000US-0236359
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                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 36.08
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-476286/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 AA;
                                                                                                                                                                                                                                                                                      WO200157270-A2.
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21-SEP-2000;
27-SEP-2000;
04-0CT-2000;
                                                                                                                                          09-0CT-2001
                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-2000;
                                                                                                                                                                                                                                                                                                                    09-AUG-2001
                                                                                                          AAM05737;
15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn SG,
                                                           AAM0573
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ဌ

Spatially-addressable set of single exon nucleic acid probes, used

Rank DR;

Chen W,

Hanzel DK,

Penn SG,

WPI; 2002-114183/15.

(MOLE-) MOLECULAR DYNAMICS INC

2000US-234687P. 2000US-236359P. 2000US-0632366.

21-SEP-2000; 27-SEP-2000; 04-OCT-2000;

03-AUG-2000; 26-MAY-2000;

2000GB-0024263

30-JAN-2001; 2001WO-US00665

04-FEB-2000;

WO200186003-A2.

15-NOV-2001

Homo sapiens

measure gene expression in human lung samples Claim 27; SEQ ID No 29583; 634pp; English.

```
The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 15014 uncleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several transcers and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the issues and/or cell types using hybridisation cell types indicates that the expression of each of the exons in the issues and/or cell types using hybridisation cell types indicates that expression of the exons in the issues and/or cell types indicates that expression of the exons in the issues and/or cell types indicates that expression of each expression of the exons in the issues and/or cell types indicates that expression of each expression of each expression of each expression of the exons in reverse and expression of each expression e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the exons should be assigned to a single gene; a peptide comprising one of 1201 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases
```

7

Gaps

٠<u>;</u>

Indels

23;

4; Mismatches

Pred. No.

23.4%; 36.0%;

5 PAIAINNPYVPRTYYANPAVVRP-HAQIPQRQYLPNSHPPTVVRRPNLHP 

δλ g ABG39918 standard; Peptide; 193 AA.

RESULT 14
ABG39918
ID ABG39
XX
AC ABG39

ABG39918;

Length 193;

Score 71.5; DB 22;

```
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PER) primers oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations
                                                                                                                                                                                                                                                               ñ
haemosiderosis, pulmonary histicoytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary cillary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fibe.
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder
                                                                                                                                                                                                                                                                                           5 PAIAINNPYVPRIYYANPAVVRP-HAQIPQRQYLPNSHPPTVVRRPNLHP 53
                                                                                                                                                                                                                                                                                                                  15 PAPAHHHP----EYQGQPVVSHPHHIMPPQQHYAPPPPPPPSHPMPHP 60
                                                                                                                                                                                                                       Score 71.5; DB 23; Length 193;
Pred. No. 0.76;
4; Mismatches 23; Indels 5
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID No 37053; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human diagnostic protein #6685.
                                                                                                                                                                                                                                                                                                                                                                                                                   ABG06694 standard; Protein; 904 AA
                                                                                                                                                                                                                       23.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                Query Match
Best Local Similarity 36.0°,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C,
                                                                                                                                                                                   193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAS70881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG06694;
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CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cannot be produce other types of data and products dependent on DNA and cannot acid sequences. ABG00010-ABG30377 represent novel human of diagnostic amino acid sequences of the invention.

CC diagnostic amino acid sequences of the invention.

Note: The sequence of this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 904 AA;

Query Match

Best Local Similarity 36.0%; pred. No. 4.5;

Matches 18; Conservative 4; Mismatches 23; Indels 5; Gaps CONSETATION PROPERTY AND AVENTY PROPRED PROPRED PROPRED PROPRED PROBLEM PROPRED PROBLEM PROPRED PROPRED PROPRED PROBLEM PROBLEM
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Search completed: August 11, 2003, 08:18:22 Job time : 41.0485 secs

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August 11, 2003, 08:16:37 ; Search time 21.8932 Seconds (without alignments) 106.293 Million cell updates/sec
                                                                                                                                                                                                                      305
1 YORRPAIAINNPYVPRTYYA......YEPNSHPPTVVRRPNLHPSF 55
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                            328717 seqs, 42310858 residues
                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                       US-09-508-095-17
                                                                                                                                                                                                   Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                   Run on:
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/cgn2\_6/ptodata/1/laa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/5B\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/AB\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/PCTUS\_COMB.pep:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Issued\_Patents\_AA:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
-	305	100.0	:	: ⊣	US-07-962-569A-8	- Care & ocaomos
7	305	100.0		н	US-08-308-883-2	, ,
m	305	100.0		-	- 1	ě c
4	305	100.0		m	US-08-256-799-2	40
S	305	100.0	182	m	US-08-462-437-2	Sequence 2, Appli
Q	298	97.7		m	US-08-462-437-31	4 (*
7	68	22.3		9	5202236-37	
80	68	22.3		φ	5202236-3	
6	67.5	22.1		m	US-09-041-886-19	. –
10	67.5	22.1		4	US-09-648-281-2	10
11	99	21.6		4	US-09-252-991A-18170	2
.12	65.5	21.5		4	US-09-252-991A-21920	
13	64	21.0		ø	5202236-7	
14	64	21.0	•	4	US-09-252-991A-16809	16809.
15	63	20.7		φ	5202236-36	Patent No. 5202236
. 16	63	20.7		9	5202236-1	No. 520223
17	63	20.7		Q	5202236-13	, c
18	Ø	20.7		ø	5202236-25	, o
19	62.5	20.5		4	US-09-252-991A-22460	2
20	62.5	20.5	628	4	US-09-252-991A-18780	
21	61.5	20.5		4	US-09-252-991A-30695	Sequence 30695. A
22	. 61	20.0		4	US-09-281-766-19	6
23	60.5	19.8		4	US-09-252-991A-21500	2150
24	60.5	19.8		4	US-09-252-991A-22366	
25	•	19.8		4	US-09-252-991A-24902	2490
56	59.5	19.5		4	US-09-252-991A-31845	Sequence 31845, A
27	59.5	19.5	726	4	US-09-252-991A-20675	20675

Segmented 10344	Segmenter 27079			Socionos 24403	Sequence 24492, A	Sequence 14, Appl	sednence 17, Appl	Sequence 12. April	Section 16743	C '0" O O O O O O O O O O O O O O O O O O O	seducince o, Appli	Sequence 29. Appl	-		rddw '67 aonanhac	Sequence 4. Appli	Sections 15		Sednence 8, Appli	Sequence 8. Appli	21,	(blin all interior
US-09-252-991A-19344	US-09-252-991A-27078	US-09-252-991A-25363	US-09-252-991A-30843	US-09-252-6018-24492	11S-07-800-364B-14	775-07-000-047-17	71-140-606 10 60	US-08-469-411-12	US-09-252-991A-16743	DCT-11991-07635-6		US-07-841-646-29	US-07-901-703-11	HS-08-147-023-20	C2 C30 C41 00 00	US-08-206-864-4	US-08-278-729A-21	0 400-100-211	0-4070-004-00 00	US-08-479-666-8	US-08-155-343A-21	
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394	476	697	663	1009	281	281	1 6	787	315	399		707	402	402		704	402	402	2	402	402	
19.3	19.3	19.2	19.0	19.0	0	0 0		T 8 . 5	18.9	18.9	0	70.7	18.9	18.9		70.7	18.9	9 8		18.9	18.9	
59	59	58.5	28	28	57.5	57.5		٥./٥	57.5	57.5	7	0.7	57.5	57.5		n .	57.5	57.5		57.5	57.5	
28	29	30	31	32	33	78		c r	36	37	ď	0	33	40	-	7	42	43	:	44	45	

## ALIGNMENTS

328717

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Length 182;
                                                                                                                                                                                                                                                                                                                      CORPUTER: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATE: US/07/962,569A
FILING DATE: 19921013
CLASSIFICATION: 435
ATTORREY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 305; DB 1;
100.0%; Pred. No. 4.6e-30;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                     ADDRESSEE: FREDERICK W. PEPPER, PH.D.
STREET: 11545 W. BERNARDO COURT, STE. 302
CITY: SAN DIEGO
               Sequence 8, Application US/07962569A; Patent No. 5391497; GENERAL INFORMATION: APPLICANT: MENON, RAVI S. APPLICANT: JEFFERS, KATHLEEN F. APPLICANT: CHANG, YING-FON APPLICANT: HAM, RICHARD G. TITLE OF INVENTION: HUMAN K-CASEIN NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 920224.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 451-1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PEPPER PH.D., FREDERICK W.
REGISTRATION NUMBER: 31,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (619) 451-9628
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 182 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 100.
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-07-962-569A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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·07-962-569A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                    STATE:
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Gaps 1 YORRPAIAINNPYVPRTYYANPAVVRPHAQIPORQYLPNSHPPTVVRRPNLHPSF 55 ö Indels ð q

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APPLICANT: Mukerji, P.
APPLICANT: Prieto, P. A.
APPLICANT: Prieto, P. A.
APPLICANT: Seo, A. E. Y.
APPLICANT: Baxter, J. H.
APPLICANT: Cummings, R.D.
TITLE OF INVENTION: Product for Inhibition of Human Rotavirus Infection.
WINDER OF SEQUENCES:
CORRESPONDENCES: ADDRESS:
ADDRESSE: Lonnie R. Drayer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb storage (B)COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh System 7.1(D)SOFTWARE: ClarisWorks 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/730,163
FILING DATE:
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                   Length 182;
                                                                                                                                                               100.0%; Score 305; DB 1;
ilarity 100.0%; Pred. No. 4.6e-30;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US/08/308,882
FILING DATE: 16-SEP-1994
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614) 624-3774
TELEFRAX: (614) 624-3074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lonnie R. Drayer
ADDRESSEE: ROSS Products Division
ADDRESSEE: Abbott Laboratories
STREET: 625 Cleveland Avenue
CITY: Columbus
                   DATE:
DOCUMENT NUMBER: PCT/W093/1519
FILING DATE: 25-JAN-1993
PUBLICATION DATE: 05-AUG-1993
RELEYANT RESIDUES IN SEQ ID NO:
US-08-308-883-2
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08730163 Patent No. 5712250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohio
: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: NO. 5712250e
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 182 amino aci
TYPE: Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
MOLECULE TYPE: Protein
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                   Query Match
Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                   US-08-730-163-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . L. Hansson et al
DNA Encoding Kappa-Casein, Process for Obtaining the Protein and Use The
             Sequence 2, Application US/08308883
Patent No. 5576300
GENERAL INFORMATION:
APPLICANT: Mikerji, P. A.
APPLICANT: Barter, P. A.
APPLICANT: Barter, J. H.
APPLICANT: Cummings, R.D.
TITLE OF INVENTION: Method for Inhibition of Human Rotavirus Infection.
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM:
MEDIUM SYSTEM: Macintosh
OPERATING SYSTEM:
SOFTWARE: ClarisMorks 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,883
FILING DATE: 16-5EP-1994
CLASSIFCATION: 435
FILING APPLICATION DATA: No. 5576300 applicable
TELECOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPAX: (614) 624-3774
TELEFAX: (614) 624-3774
TELEFAX: (614) 624-3774
TELEFAX: (614) 624-3074
TELEFAX: (614) 624-3074
TELEFAX: MST ST OID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: Amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                   Lonnie R. Drayer
ROSS Products Division
Abbott Laboratories
                                                                                                                                                                                                                                                                                                        STREET: 625 Cleveland Avenue CITY: Columbus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
ATTHORS: L. HAISSON ET
                                                                                                                                                                                                                                                                                                                                                        STATE: Ohio
COUNTRY: United States
ZIP: 43215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear
MOLECULE TYPE: Protein.
DESCRIPTION:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POSITION IN GENOME:
CHROMOSOME/SEGMENT
MAP POSITION:
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TISSUE TYPE:
CELL TYPE:
CELL LINE:
CELL LINE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                         ADDRESSEE:
ADDRESSEE:
                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
US-08-308-883-2
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: STROEMQVIST, Mats
APPLICANT: BERGSTROEM, Sven
APPLICANT: BERGSTROEM, Sven
APPLICANT: TOERRELL, Jan
TITLE OF INVENTION: DNA ENCODING KAPPA-CASEIN, PROCESS
TITLE OF INVENTION: POR OBTAINING THE PROTEIN AND USE THEREOF
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND THE TOER THEREOF
STREET OF THE TOER THE TOER THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,437
FILING DATE: 05-JUN-1995
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: DK 88/92
FILING DATE: 23-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                 ; DB 3;
4.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 305; DB 3; Best Local Similarity 100.0%; Pred. No. 4.6e-30; Matches 55; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 419 Seventh Street, N.W., Suite 300 CITY: Washington
                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                    ilarity 100.0%; Score 305; Conservative 0; Mismatcher
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-462-437-2; Sequence 2, Application US/08462437; Patent No. 6232094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-PC-
SOFTWAPP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPRAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FELECOMMUNICATION INFORMATION:
                                                                                                       1: 182 amino acids
amino acid
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202-737-3528
                                                                                                                                                            / MOLECULE TYPE: protein US-08-256-799-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                               linear
                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 55; Conserv
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TELEX: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-462-437-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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DNA Encoding Kappa-Casein, Process for Obtaining the Protein and Use The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 100.0%; Score 305; DB 1; Length 182; Similarity 100.0%; Pred. No. 4.6e-30; 55; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: TROEMOVIST, Mats
APPLICANT: STROEMOVIST, Mats
APPLICANT: STROEMOVIST, Mats
APPLICANT: BERGSTROEM, Sven
APPLICANT: HENELL, Olle
APPLICANT: Toernell, Jan
TITLE OF INVENTION: DNA ENCODING KAPPA-CASEIN, PROCESS FOR
TITLE OF INVENTION: OBTAINING THE PROTEIN AND USE THEREOF
CORRESPONDENCES: 26
CORRESPONDENCES: 26
CORRESPONDENCES: BROWDY AND NEIMARK
AUDRESSEE: BROWDY AND NEIMARK
AUDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: COOPER, IVER P. REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: HANSSON-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CUCRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,799
FILING DATE: 06-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                             DOCUMENT NUMBER: PCT/W093/15196
FILING DATE: 25-JAN-1993
PUBLICATION DATE: 05-AUG-1993
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08256799 Patent No. 6222094
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                                                                                                                                                                                                       LOCATION:
LOCATION:
LOCATION:
OTHER INFORMATION:
PUBLICATION INFORMATION:
'''MUORS: L. HAISSON ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 23-JAN-1992
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: D
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                          POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 55; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
        ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                              JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-730-163-2
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                                                                           CLONE:
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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                                                                           LENGTH: 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
ZIP: 92122
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                                                             SEQ ID NO:37:
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                                                                                               5202236-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YORRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 55
                                                                                                                                                                                                                        APPLICANT: TOERNELL, Jan
TITLE OF INVENTION: DNA ENCODING KAPPA-CASEIN, PROCESS
TITLE OF INVENTION: FOR OBTAINING THE PROTEIN AND USE THEREOF
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Patent NO. 5202236
; APPLICANT: MAUGH, KATHY J.;ANDERSON, DAVID M.;STRAUSBERG,
;SUSAN L.;MCCANDLISS, RUSS;WEI, TENA;FILPULA, DAVID
TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 298; DB 3;
Pred. No. 3.3e-29;
                                                                                                                                                                                                                                                                                                                       E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/462,437
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 88/92
FILING DATE: 23-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
                                                                                           Sequence 31, Application US/08462437; Patent No. 6212094; GENERAL INFORMATION:
APPLICANT: HANSSON, Lennart
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: COOPER, IVER P. REGISTRATION NUMBER: 28,005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: HP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                    APPLICANT: STROEMQVIST, MALS
APPLICANT: BERGSTROEM, Sven
APPLICANT: HERNELL, Olle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 933,945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 182 amino acids
                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND

// MOLECULE TYPE: protein
US-08-462-437-31
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Best Local Simi
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                                                     RESULT 6
US-08-462-437-31
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COUNTRY:
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CITY: Wa
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130 YKAKPIYKI-KPIYPSIYKAKPINPSIYKAKPSYPPIYKAKPSYPPIYKAKPSYPPIY 186
                                                                                                                                                                                                                                                                                                                        1 YORRPAIAINNPYVPRTYYA---NPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 55
                                                                                                                                                                                                                                                                                        1 YORRPAIAINNPYVPRTYYA---NPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 55
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                                                                                                                                                                                      DB 6; Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5202236

** APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG,

** SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID

** TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                    28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Deperiture OF INVENTION: Polypeptides and Methods of NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 70
CITY: San Diego
STATE: California
                                                                                                                                                                                Score 68; DB 6;
Pred. No. 0.95;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.3%; Score 68; DB 29.3%; Pred. No. 0.96 iive 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1967
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1966
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/09/041,886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
                                                                                                                                                                                Query Match 22.3%;
Best Local Similarity 29.3%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States
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Matches 17; Conservative
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PAPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YORRPAIAIN---NPYVPRTYYANPAVVRPHAQIPQRQYLPN----SHPPTVVRRPNLH 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 YKAKPSYPPTYKAKPTYPSTYKAKPSY--PPTYKPKISYPPTYKAKPSYPPTYKAKPSYP
                                                        Gaps
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                                                        4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ORRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYL----PNSHPPTVVR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 822;
              DB 4; Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6; Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25; Indels
                                                                                                             49
                                                                                  10 NNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRP
                                                 4; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 65.5; DB
Pred. No. 5.5;
5; Mismatches
        Score 66; DB Pred. No. 1.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                         Sequence 21920, Application US/09252991A abstent No. 6551795
GENERAL INFORMATION: APPLICANT: MARC J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 39
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY 1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
        21.6%;
35.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 933,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.5%;
Best Local Similarity 30.8%;
Matches 20; Conservative
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      Query Match 21.69
Best Local Similarity 35.09
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 24-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
SEQ ID NO 21920
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90 PDLQP 94
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Pulst, Stefan M.
TITLE OF INVENTION: Transgenic Animal Model of
TITLE OF INVENTION: Neurodegenerative Disease and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        э,
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Pred. No. 5.4;
3; Mismatches 18; Indels 3
                                                                                                                                                                                                                                                                                   Length 1312;
                                                                                                                                                                                                                                                                                                                       18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Indels
                                                                                                                                                                                                                                                                                                                                                                                     563 PSRYQSGPNSLPPRAATPTR---PPSRPPSRPSHPS 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 PRIYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPS 54
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                                                                                                                                                                                                                                                                                   DB 3;
                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/648,281
CURRENT FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 12
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ER: US 60/074,788
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                                 REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPRONE: (619) 535-9001
TELEPRAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18170, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09648281
Patent No. 6315197
GENERAL INFORMATION:
APPLICANT: Pulst, Stefan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.1%;
40.0%;
                                                                                                                                                                                                                                                                               22.1%;
                                                                                                                                                           1312 amino acids
                                                                                                                                                                                                                                                                                                Best Local Similarity 40.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 40.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-CE 4336
NAME: Campbell, Cath REGISTRATION NUMBER:
                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-09-041-886-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapien
US-09-648-281-2
                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SEQ ID NO 18170
                                                                                                                                                                                                   linear
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US-09-252-991A-18170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . LENGTH: 1312
                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-09-648-281-2
                                                                                                                                                           LENGTH:
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Search completed: August 11, 2003, 08:19:44 Job time : 22.8932 secs
                                                                                                                                                                                    RESULT 14

US-09-252-991A-16809

Sequence 16809, Application US/09252991A

Factor No. 6551795

GENERAL INFORMATION:

APPLICAMT:

APPLICAMT
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3 RRRPARSPAHPEPVPPTYRHDHRAATPRRRAHSGVNCDEPRDFLVPSHPRRRPLPGHHPG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------ 43
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**PPLICANT: MAGGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, SON L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID

**TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QRRPAIAINNPY-VPRTYYANPAVVRP----HAQI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 64; DB 4;
Pred. No. 6.9;
8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YQRRPAIAINNPYVPRTYYANPAV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PELLING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16809
LENGTH: 691
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAX-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16809
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FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
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FILING DATE: 07-AUG-1987
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Best Local Similarity 30.99
Matches 21; Conservative
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PTY 64
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PSF
                                                                             62
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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 11, 2003, 08:17:06; Search time 151.65 Seconds Run on:

(without alignments)
46.167 Million cell updates/sec

US-09-508-095-17 305 1 YORRPAIAINNPYVPRTYYA......YLPNSHPPTVVRRPNLHPSF Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

479057 segs, 127295195 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published\_Applications\_AA:\*

ptodata/1/pubpaa/USO9B\_PUBCOMB.ppp: ptodata/1/pubpaa/USO9C\_PUBCOMB.pep: ptodata/1/pubpaa/USO9\_NEW\_PUB.pep:\* ptodata/1/pubpaa/US10A\_PUBCOMB.pep: ptodata/1/pubpaa/US10B\_PUBCOMB.pep: ptodata/1/pubpaa/US10C\_PUBCOMB.pep: oubpaa/US09A\_PUBCOMB.pep ptodata/1/pubpaa/US10\_NEW\_PUB.pep Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:<sup>,</sup> /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:<sup>,</sup>

## SUMMARIES

Poen 1+						
NO.	Score	Match I	Watch Length DB	В	Ω	Description
-	76.5	25.1	413	14	US-10-062-254-270	Sequence 270, App
7	71.5	23.4	193	σ	US-09-864-761-37748	Sequence 37748. A
e	65	21.3	425	14	US-10-062-254-274	Sequence 274. App
4	63.5	20.8	351	14	US-10-029-217A-7	Sequence 7, Appli
ι.	63	20.7	81	15	US-10-083-357-1283	Sequence 1283. Ap
9	61	20.0	865	10	US-09-957-995A-19	Segmence 19. Appl
. 7	60.5	19.8	09	10	US-09-816-669A-10	Segmence 10 Appl
80	58.5		462	10	US-09-974-298-151	Section 151 App
σ	58.5		462	12	US-10-043-487-349	Sequence 349. Ann
10	58		366	101	US-09-801-368-254	Sequence 254. App
11	57.5		402	60	US-08-957-425-29	Sequence 29. Appl
12	57.5		402	ω	US-08-260-675-21	Sequence 21, Appl
13	57.5		402		US-10-122-026-6	Sequence 6, Appli
14	57.5		402	15	US-10-050-050-21	Sequence 21, Appl
15	57.5		403	10	US-09-813-398-31	Sequence 31, Appl

Sequence 254, App	Sequence 46, Appl	46,	101	2	_	, y	9	8173	, 0,		261,	e 98,	87,	1396	276	148	e 148	96	Sequence 50, Appl	15	40,	Sequence 40, Appl	41,	41,	42,	42,	e 1567,	Sequence 36101, A	a 2200,
4 US-10-062-	us-09-202-	9 US-09-844-353A-46	US-09-844-	ns-09-903-	-6EL-60-SD	9 US-09-906-179-5	ហ	15 US-10-128-714-8173	1 US-09-98	9 US-09-764-853-772	US-09-764-898-26		15 US-10-073-865-87	US-09-764-	us-10-062-	_		US-09-764	-10-146	us-10-160-	Φ	US-09-844-3	9 US-09-205-658-41	9 US-09-844-353A-41	9 US-09-205-658-42	9 US-09-844-353A-42	10 US-09-764-877-1567	-SD	12 US-10-017-16j-2200
420	509	509	635	919	180	369	662	671	199	315	315	315	315	363	409	474	474	935	2971	4349	196	964	828	828	892	892	171	190	282
18.9	18.9	18.9	18.9	18.9	18.7	18.7	18.7	18.7	18.5	18.5	18.5	18.5	18.5	18.5	18.5	18.5	18.5	18.5	18.5	18.5	18.4	18.4	7		18:4	œ	18:2	18.2	18.2
57.5	57.5	57.5	7	7		57		57	56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5	ė.	56	26	26	26	26	26	δ.	55.5	55.5
16	17	18	19	20.	21	22	23	24	. 25	56	27	28	58	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

RESULT 1

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																			Proteins
																			Encoding
US-10-062-254-270	Sequence 270, Application US/10062254	Publication No. US20020138882Al.	GENERAL INFORMATION:	APPLICANT: Cahoon, Edgar B	APPLICANT: Cahoon, Rebecca E	APPLICANT: Falco, Saverio Carl	APPLICANT: Fang, Yiwen	APPLICANT: Hantke, Sabine S.	APPLICANT: Lee, Jian-Ming	APPLICANT: Li, Zhongsen	APPLICANT: Miao, Guo-Hua	APPLICANT: Morgante, Michele	APPLICANT: Niu, Xiping	APPLICANT: Odell, Joan	APPLICANT: Rafalski, Antoni	APPLICANT: Sakai, Hajime	APPLICANT: Zheng, Peizhong	APPLICANT: Zhu, Qun	TITLE OF INVENTION: Polynucleotides Encoding Proteins 1
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Proteins Involved In Plant Metabolism CURRENT APPLICATION NUMBER: US/10/062,254 PRIOR APPLICATION NUMBER: 09/630,346
PRIOR PILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/146511
PRIOR APPLICATION NUMBER: 60/15606
PRIOR APPLICATION NUMBER: 60/15606
PRIOR PILING DATE: 1999-09-23
PRIOR PELING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/156899
PRIOR PILING DATE: 1999-09-07
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16

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ITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 PAIAINNPYVPRTYYANPAVVRP-HAQIPOROYLPNSHPPTVVRRPNLHP 53
                                                                                                                                                                                                                                                                                                                      EXPRESSED IN HEART, SIGNAL - 1.2
EXPRESSED IN HBL100, SIGNAL - 2.1
EST_HUMAN HIT: AA831893.1, EVALUE 7.00e-07
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 71.5; DB 9; Length 193; Pred. No. 1.1; 4; Mismatches 23; Indels
                            SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 37748 LENGTH: 193
                                                                                                                                                                                                                                        EXPRESSED IN PLACENTA, SIGNAL = EXPRESSED IN BRAIN, SIGNAL = 1 EXPRESSED IN LUNG, SIGNAL = 1.4 EXPRESSED IN BORE MARROW, SIGNAL = 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/062,254 CURRENT FILING DATE: 2002-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/10062254
o. US20020138882A1
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APPLICATION NUMBER: 09/630,346
FILING DATE: 2000-07-28
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APPLICATION NUMBER: 60/157287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/169767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/172958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/171515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60/173535
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Falco, Saverio Carl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1999-12-09
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Lee, Jian-Ming
Li, Zhongsen
Miao, Guo-Hua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-10-0
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 36.08
Matches 18; Conservative
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Rafalski, Antoni
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Sheng, Peizhong
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                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xiping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Onu
                                                                                                                                                          OTHER INFORMATION:
             NUMBER OF SEQ ID
                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATIONS-09-864-761-37748
                                                                                             TYPE: PRI
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PPLICANT: Hanzel, David K.
PPLICANT: Chen, Wensheng
ITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                 Length 413;
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                      2 ORRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTV 45
                                                                                                                                                                                                                                                                                                                                                                                                       22 ROSPAVARPQGWVPMQYPAAAAWWPHHMLPPQHYAP---PPYV 62
                                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                          Score 76.5; DB
Pred. No. 0.68;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JRRENT APPLICATION NUMBER: US/09/864,761
JRRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLICATION NUMBER: PCT/US01/00668
LING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/180,312
FILING DATE: 2000-02-04
APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLICATION NUMBER: PCT/US01/00664
LING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/207,456
FILING DATE: 2000-05-26
APPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NG DATE: 2000-10-04
LICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ION NUMBER: PCT/US01/00663
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FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 37748, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILLING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
                   FILING DATE: 1999-12-21
APPLICATION NUMBER: 60/171515
FILING DATE: 1999-12-22
                                                      PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: 60/173535
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 375
SOFWARE: MICROSOft Office 97
SEQ ID NO 270
LENGTH: 413
APPLICATION NUMBER: 60/172958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                      Query Match 25.1
Best Local Similarity 38.6
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                         ; ORGANISM: Glycine max US-10-062-254-270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LING DATE: 2
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                                                                                                                                                                                                       TYPE: PRT
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APPLICANT: Conrad, Patricia A.
Barr, Bradd C.
Anderson, Mark L.
Sverlow, Karen W.
TITLE OF INVENTION: Recombinant Neospora Antigens and Their
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                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 023070-082512US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 21-MAR-1994
APPLICATION NUMBER: US 08/327,516
FILING DATE: 20-OCT-1994
APPLICATION NUMBER: US 08/645,951
FILING DATE: 10-MAY-1996
FILING DATE: 10-MAY-1996
FILING DATE: 30-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/957,9958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/215,858
                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           771 SRSRLPSAVEPSPPASPQPSPHPS 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
                                                                            Sequence 19, Application US/09957995A Patent No. US20020165373A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 15-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 QRQYLPNS---HPPTVVRRPNLHPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 865 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                         STATE: California
                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: OLSON, ERIC N.
APPLICANT: WANG, DA-ZHI
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO A CARDIAC-SPECIFIC
TITLE OF INVENTION: NUCLEAR REGULATORY FACTOR
FILE REFERENCE: UTSD:695US
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                          Score 65; DB 14; Length 425;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                         2 ORRPAIAINNPYVPRTYYANPAVVRPHAQIPORQYLPNSHPPTV 45
                                                                                                                                                                                                                                                  Length 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 NPYVPRTYYANPAVVRPHAQIPQRQYLPNS-----HPPTVV 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Qiandong Zeng et al.
TITLE OF INVENTION: Systemic Discovery of New Genes FILE REFERENCE: 03296-090
CURRENT APPLICATION NUMBER: US/10/083,357
CURRENT FILING DATE: 2002-02-27
NUMBER OF SEQ ID NOS: 1346
SEQ ID NO 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
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Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.8%; Score 63.5; DB
33.3%; Pred. No. 17;
tive 8; Mismatches
                                                                                                                                                                                            8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/029,217A CURRENT FILING DATE: 2002-03-19 PRIOR APPLICATION NUMBER: 60/257,761 NUMBER OF SEQ ID NOS: 32 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1283, Application US/10083357
Publication No. US20030054370Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/10029217A Publication No. US20020164735A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Saccharomyces cerevisiae US-10-083-357-1283
                                                                                                                                                Query Match
Best Local Similarity 36,4%;
Matches 16; Conservative
NUMBER OF SEQ ID NOS: 375
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.7%;
31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 33.39
Matches 16; Conservative
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Best Local Similarity 31.87
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT-
ORGANISM: Mus musculus
                                                                                            ; ORGANISM: Glycine max US-10-062-254-274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IS-10-083-357-1283
                                                                                                                                                                                                                                                                                                                                     US-10-029-217A-7
                                       SEQ ID NO 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-029-217A-7
                                                                            TYPE: PRT
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112 YGRDPCPCASHPYPADDSPLGSYAPDPSPPGSYPPEPSPSKPSPPEGSSPRVPSPHRH-P 770 Gaps 32; Indels 20.0%; Score 61; DB 10; 24.7%; Pred. No. 84; tive 10; Mismatches 22 ----VPRTY----Sequence 10, Application US/09816669A Patent No. US20020137019A1 GENERAL INFORMATION: APPLICANT: GARABEDIAN, Michael

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TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypep TITLE OF INVENTION: mammalian polypeptides
FILE REFERENCE: B4778A
CURRENT APPLICATION NUMBER: US/10/043,487
CURRENT FILING DATE: 2002-04-30
PRIOR PPLICATION NUMBER: WS 60/261,130
PRIOR PPLICATION NUMBER: 2001-01-12
NUMBER OF SEQ ID NOS: 561
SOFTWARE: PAENTIN version 3.1
LENGTH: 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                        44 INLPFVQRETPNAYANVAQLATSPTQAKSGYYCRYYAVPFPTYPQQPQSPYQQAVLPYAT 103
                                                                                                                                                                                                                                                                                                                                                                                                ----PYVPRTYYANPAVVRP-----HAQIPQRQYLPNSHPPT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --- AVVRPHAQ 30
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                                                                                                                                                                                                                                                                                                                     Length 462;
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                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                 DB 15;
                                                                                                                                                                                                                                                                                                                                                          26;
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73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                 Score 58.5; 1
Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION UNMBER: US/U9/801,368
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR PLILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
LENGTH: 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.0%; Score 58; 23.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. US20020128250Alman, Thea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 254, Application US/09801368 Patent No. US20020128250A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Saccharomyces cerevisiae US-09-801-368-254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 IPQRQYLPNSHPPTVVRRP-
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 28.6%;
Matches 20; Conservative
                                                                                                                                                                                                                                                   ORGANISM: Shigella Flexneri
US-10-043-487-349
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Matches 22; Conservative
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Madden, Kevin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Silva, Jeff
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                                  APPLICANT: MARKUS, Steven
TITLE OF INVENTION: AETHOD FOR SCREENING TRANSCRIPTIONAL COREGULATORY PROTEINS OF
TITLE OF INVENTION: MATHOD FACTORS, AND ANDROGEN RECEPTOR TRANSCRIPTIONAL CG
TITLE OF INVENTION: PROTEINS AS TARGETS FOR ANDROGEN RECEPTOR-DEPENDENT DISEASES
FILE REFERENCE: GARABEDIAN-1.1A
CURRENT APPLICATION NUMBER: US/09/416,669A
CURRENT APPLICATION NUMBER: 60/225,618
PRIOR FILING DATE: 2000-08-15
PRIOR FILING DATE: 2000-08-15
PRIOR FILING DATE: 2000-03-24
NUMBER: OF SEQ ID NOS: 20
SOFTWARE: PATCHIN VERSION 3.1
SEQ ID NO 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---PYVPRTYYANPAVVRP----HAQIPQRQYLPNSHPPT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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; OTHER INFORMATION: Incyte ID No. US20020156263A1 2716815CD1
US-09-974-298-151
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GENERAL INCOLOLISABIAI
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
CURRENT FILING DATE: 2001-10-04
PRIOR RPLICATION NUMBER: 60/238,331
PRIOR RPLICATION NUMBER: 60/238,331
PRIOR RPLICATION NUMBER: 60/238,331
SOFTWARE: PERL PROGRE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 60.5; DB 10;
Pred. No. 5.5;
9; Mismatches 16;
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Pred. No. 82;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 319, Application US/10043487; Publication No. US20030055220A1
GENERAL INFORMATION: APPLICANT: HYBRIGENICS
APPLICANT: PIERTE, LEGRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 151, Application US/09974298
Patent No. US20020156263A1
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28.6%;
                   HITTELMAN, Adam
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Best Local Similarity 33.3
Matches 16; Conservative
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Best Local Similarity 28.6
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Human
US-09-816-669A-10
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STREET: 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27, 829
REFERENCE/DOCKET WUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                          PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/957,425 FILING DATE: 24-Oct-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/447,570
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FILING DATE: 23.FEB-1989
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 21-FEB-1992
APPLICATION NUMBER: US 810,560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILING DATE: 28-JAN-1992
PPLICATION NUMBER: US 660,162
ILING DATE: 22-FEB-1991
                                                                                                             OZKAYNAK, ENGIN
KUBERASAMPATH, THANGAVEL
RUEGER, DAVID C.
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PPLICATION NUMBER: US 827,052
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PLICATION NUMBER: US 616,374
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PPLICATION NUMBER: US 599,543
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PPLICATION NUMBER: US 579,865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 07-SEP-1990
APPLICATION NUMBER: US 569,920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
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                     Sequence 29, Application US/08957425
Publication No. US20030069401A1
GENERAL INFORMATION:
APPLICANT: OPPERMANN, HERMANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILING DATE: 20-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'ILING DATE: 17-0CT-1989
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LENGTH: 402 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                         STATE: MASSACHUSETTS COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LING DATE: 04-DEC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      CITY: BOSTON
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08-957-425-29
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-----QIPQRQYLP-----NS 40
                                                                                                                                                                       Gaps
                                                                                                                                                                   23;
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APPLICANT: RUEGER, DAVID C
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OPSERVINAK, ENGIN
APPLICANT: OCKAYNAK, ROGIN
APPLICANT: COHEN, CHARLES M
TITLE OF INVENTION: MORPHOGEN-INDUCED NERVE REGENERATION AND
TITLE OF INVENTION: REPAIR
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                         Length 402;
                                                                                                                                                                   Indels
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CURRENT APPLICATION DATA:
                                                                                                                           DB 8;
                                                                                                                       18.9%; Score 57.5; Ilarity 29.3%; Pred. No. 92; Conservative 8; Mismatches
                                                                                                                                                                                                  2 QRRPAIAINNPYVPRTYYANPAVVR-PHA----
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-08-957-425-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: TESTA HURWITZ & THIBEAULT 55 STATE STREET
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APPLICATION NUMBER: US 07/667,274
FILING DATE: 11-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/752,764
FILING DATE: 30-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/126,100
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/922,813
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/08260675
Publication No. US20030104993A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                           41 HPPTVVRRPNLHPSF 55
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SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino act
                                                                                                                     Query Match
Best Local Similarity
Matches 22; Conserv
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TOPOLOGY:
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Gaps

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-----OIPOROYLP-----NS 40
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ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
                                                                                                                                                                    Length 402;
                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROLIFERATION OF EPITHELIAL CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                    DB 15;
                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART, JOHN E.
TITLE OF INVENTION: MORPHOGEN TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: FENTON ESQ., GILLIAN M. REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-074DV
                                                                                                                                                                                                           8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/461,113
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: US 08/445,882
FILING DATE: 22-WAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/10/050,050
FILING DATE: 15-Jan-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                  18.9%; Score 57.5; 29.3%; Pred. No. 92
                                                                                                                                                                                                                                              2 QRRPAIAINNPYVPRTYYANPAVVR-PHA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-10-050-050-21
                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: COHEN, CHARLES M.
CHARETTE, MARC F.
KUBERASAMPATH, THANGAVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/10050050 Publication No. US20030125230A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , HERMANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FELEPHONE: (508) 435-900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
                              LENGIH: 402 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PANG, ROY H.L.
OZKAYNAK, ENGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RUEGER, DAVID C. OPPERMANN, HERMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                               296 HGRQVCRRHELYVSF 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 01748
COMPUTER READABLE FORM:
                                                 TYPE: amino acid
                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: HOPKINTON
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                                                                                                                                                                                Best Local Similarity
Matches 22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                             US-10-122-026-6
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                                                                                                          Gaps
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OZKAYNAK, ENGIN
KUBERASMPATH, THANGAVEL
TITLE OF INVENTION: NOVEL MORPHOGENIC PROTEIN COMPOSITIONS
OF MATTER
                                                                 Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Administrator, Testa, Hurwitz &
                                                                                                      Indels
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                                                                                                      22;
                                                               DB 8;
                                                                                                      8; Mismatches
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APPLICATION NUMBER: US 07/971,091
PRITING DATE: 03-NOV-1993
                                                                                  Pred. No. 92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 28-AUG-1992
APPLICATION NUMBER: US 07/923,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 31-JUL-1992
APPLICATION NUMBER: US 07/752,857
FILING DATE: 30-AUG-1991
APPLICATION NUMBER: US 07/752,764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/122,026
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                                                               Score 57.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                       2 QRRPAIAINNPYVPRTYYANPAVVR-PHA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: CAMACHO, JENNIFER A. REGISTRATION NUMBER: 43,526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thibeault, LLP STREET: 125 HIGH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 29-Aug-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 30-AUG-1991
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                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/10122026
Publication No. US20030105004A1
                                                                                                                                                                                                                                                                                                                                                                         Dilication NO. C. GENERAL INFORMATION:
APPLICANT: JONES, WILLIAM K
TUCKER, RONALD F
RUEGER, DAVID C
RUEGER, DAVID C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                        296 HGROVCRRHELYVSF 310
                                                           Query Match
Best Local Similarity 29.3%;
Matches 22; Conservative
                                                                                                                                                                                                                   41 HPPTVVRRPNLHPSF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Flopp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
; MOLECULE TYPE: protein US-08-260-675-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOSTON
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-----QIPQRQYLP-----NS 40
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                                           Gaps
                                         23;
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   DB 15; Length 402;
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                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                     Sequence 31, Application US/09813398
Fatent No. US20020169292A1
GENERAL INPORMATION:
APPLICANT: Bruce D. Weintraub
APPLICANT: University of Maryland
TILE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
FILE REFERENCE: UOFMD.003C1
CURRENT FILING DATE: 2001-03-20
PRIOR PAPLICATION NUMBER: PCT/US99/05908
PRIOR APPLICATION NUMBER: PCT/US99/05908
PRIOR APPLICATION NUMBER: PCT/US99/05908
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-19
STOR FILING DATE: 1998-09-22
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 00-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
 Score 57.5; DB; Pred. No. 92; B; Mismatches
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Best Local Similarity 29.3%; Pred. No. 92;
Matches 22; Conservative 8; Mismatches
                                                                        2 QRRPAIAINNPYVPRTYYANPAVVR-PHA----
Query Match
Best Local Similarity 29.3%;
Matches 22; Conservative 8
                                                                                                                                                                     41 HPPTVVRRPNLHPSF 55
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CORGANISM: HOMO SAPIEN
US-09-813-398-31
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Search completed: August 11, 2003, 08:25:41 Job time: 151.65 secs

41 HPPTVVRRPNLHPSF 55

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

August 11, 2003, 08:16:37 ; Search time 14.9515 Seconds (without alignments) 353.763 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-508-095-17 305 1 YORRPAIAINNPYVPRTYYA......VLPNSHPPTVVRRPNLHPSF 55

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283308 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	KKHU	A48382	KKGT	S15513	KKBOB	KKSHA	JC4955	S12092	T06482	WMBEL1	S52985	AB2067	523760	T52359	T25073	T40619	240047	300937	A/2430	819129	AH2891	D97667	H71332	S19150	<b>T40820</b>	T10064	C81704	100532	T52340	ന	
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	Length	182	188	171	192	190	192	180.	234	352	340	381	289	875	1400	254	735	751	101	017	340	/09	044	516	628	238	329	506	753	306	636	
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T34918	S10015	T40493	A44282	T16232	T06576	T04449	J01663	B96591	T52078	T14171	C64228	S37864	S51302	AE0369	T15525
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19	19	19	19	19	19	19	19	13	13	19.2	19	19	19	19	18
09	59.5	59.5	59.5	59.5	59.5	29	58.5	58.5	58.5	58.5	58	28	58	58.	57.5
30	31	32	33	34	35	36	3.7	38	39	40	41	42	43	44	4.5

# ALIGNMENTS

32 .; Stroemqvi	Rigiat, A.M.; Jolles, J.; Aubert, J.P.; Loucheux-Lefebvre, M.H.; Jolles, we have the N. Filat, A.M.; Jolles, J.; Aubert, J.P.; Loucheux-Lefebvre, M.H.; Jolles, P. Eur. J. Biochem. 111, 333-399, 1980  A.Title: Localisation and importance of the sugar part of human casein. A.Reference number: Al6604; MUID:81114144; PMID:7460900  A.Accession: Al6604  A.Molecule type: protein A.Residues: 118-160, TT', 163-172, 'P', 174-177, 'PTTS', 182 <fia> C.Comment: This protein is only a minor component in human milk, whereas it is a cows C.Genetics: A.Gene: GBB:5316337; OMIM:601695  A.Gene: GBB:CSN10; cask; CSN3; Kca A.Gene: GBB:CSN10; cask; CSN3; Kca A.Gene: GBB:CSN10; cask; CSN3; CA A.Map Position: 4421.1 A.Introns: 18/3; 29/3 A.Note: the first intron occurs before the initiator codon C.Superfamily: Rappa-casein C.Keywords: 91ycoprotein; mammary gland; milk; pyroglutamic acid F:1-22/Domain: signal sequence #status predicted &lt;510&gt; F:21-182/Product: kappa-casein #status experimental <amt></amt></fia>
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Gaps

.; %

21; Indels

Score 129; DB 1; Pred. No. 1.8e-07; 6; Mismatches 21

42.3%;

Length 171;

22

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C;Comment: Chymosin hydrolyzes the peptide bond between Phe-105 and Met-106.
C;Superfamily: kappa-casein
C;Keywords: mammary gland; milk; phosphoprotein
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                                                                                                                                    Llarity 44.4%;
Conservative
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A; Residues: 1-190 <STE>
                                                                                                                                    Local Similarity
les 28; Conserv
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A; Residues: 1-192 <COL>
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F;118-182/Product: caseinoglycopeptide #status experimental <CGP>
F;23/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment
F;117-118/Cleavage site: Phe-Tle (chymosin) #status experimental
F;113-143,148,151,157,169,178,181/B1/Binding site: carbohydrate (Thr) (covalent) #statu
F;162/Binding site: carbohydrate (Ser) (covalent) #status experimental
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A; Residues: 1-188 <LEV>
A; Cross-references: GB:X51977; GB:S42402; NID:g406774; PIDN:CAA36239.1; PID:g406775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Sus scrofa domestica (domestic plg)
C; Date: 19-Nov.1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
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C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Dec-2000
C;Accession: A94479; A90670; A03114
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A; Molecule type: protein
A; Note: 1-171 < MEI>
A; Note: Me amino-terminal residue appears to be pyrrolidone carboxylic aci
R; Mercier, J.C.; Addeo, F.; Pelissier, J.P.
Biochimie 58, 1303-1310, 1976
A; Title: Structure primaire du caseinomacropeptide de la caseine K caprine.
A; Reference number: A90670; MUID: 77112689; PMID: 1016651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A. Experimental source: mammary gland
A. Note: sequence extracted from NCBI backbone (NCBIN:110878, NCBIP:110880)
R. Chobert, J. M.; Mercher, J.C.; Bahy, C.; Haze, G.
FEBS Lett. 72, 173-178, 1976
A.Title: Structure primaire du caseinomacropeptide des caseines kappa porc
A. Reference number: A12717; MUID:77068846; PMID:1001463
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A;Title: Cloning and sequencing of the porcine kappa-casein cDNA. A; Reference number: 448382; MUID:9236799; PMID:1503275
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Pred. No. 6.4e-11;
5; Mismatches 20;
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                                                                                                                                                                 Score 305; DB 1;
Pred. No. 2.8e-27;
                                                                                                                                                              th 100.0%; Score 305; D. Similarity 100.0%; Pred. No. 2.8 55; Conservative 0; Mismatches
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A; Residues: 106-171 (AME2>
Note: 119-Val was also found
A; Note: Ser-151 and Ser-168 are phosphorylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 54.5%;
Matches 30; Conservative
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A; Residues: 118-188 <CHO>
C; Superfamily: kappa-casein
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R; Levine, W.B.; Alexander, 1
                                                                                                                                                                                          Best Local Similarity
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C; Species: Bos primigenius taurus (cattle)
C; Date: 24-Apr-1984 #sequence_revision 23-Mar-1995 #text_change 16-Jun-2000
C; Date: 24-Apr-1984 #sequence_revision 23-Mar-1995 #text_change 16-Jun-2000
C; Accession: 302076; B22071; 306376; JN0364; A91206; A90033; A90920; A91634; A90592;
R; Alexander, L.J.; Stewart, A.F.; MackInlay, A.G.; Kapelinskaya, T.V.; Tkach, T.M.; C Eur. J. Biochem. 178, 395-401, 1988
A; Title: Isolation and characterization of the bovine kappa-casein gene.
A; Contents: A variant
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                                                                                                                                                                                                                                                                                                                                                                          C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Aug-1999
C;Accession: S15513
S;Coll, A.; Folch, J.M.; Sanchez, A.
submitted to the EMBL Data Library, July 1991
A;Reference number: S15513
A;Accession: S15513
A;Status: preliminary
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A; Residues: 1-190 cALE:
A; Residues: 1-190 cALE:
A; Cross-references: EMBL:X14907; NID:g177; PIDN:CAA33034.1; PID:g1228078
R; Stewart, A.F.; Willis, I.M.; Mackinlay, A.G.
R; Stewart, A.F.; Willis, I.M.; Mackinlay, A.G.
A; Stewart, A.F.; Willis, I.M.; Mackinlay, A.G.
A; Title: Nucleotide sequences of bovine alpha-s1- and kappa-casein cDNAs.
A; Reference number: A93517; MUID:84221403; PMID:6328443
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R;Gorodetskii, S.I.; Kaledin, A.S.
Sov. Genet. 23, 398-404, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X60763; NID:9977; PIDN:CAA43174.1; PID:9978
C;Superfamily: kappa-casein
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44.4%; Pred. No. 2e-07;
ive 6; Mismatches 21; Indels
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Best Local Similarity 44.4%;
Matches 28; Conservative
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A; Molecule type: mRNA
A; Residues: 1-192 <CROTA
A; Cross-references: EMBL.X51822; NID:91293; PIDN:CAA36122.1; PID:91294
A; Johles, J.; Schoentgen, F.; Hermann, J.; Alais, C.; Jolles, P.
Eur. J. Blochem. 46, 127-132, 1974
A; Title: The sequence of sheep kappa-casein: primary structure of para-kappa-A-casein
A; Reference number: A91221; MUID:74309256; PMID:4605338
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A; Residues: 22. (0'.24-27, 'E', 29-129 <JOL1>
B; Jolles, J.; Flat, A.M.; Schoentgen, F.; Alais, C.; Jolles, P.
Biochim. Blophys. Acta 365, 335-343, 1974
A; Tile: The amino acid sequence of sheep kappa-A-casein. II. Sequence studies concer A; Reference number: A90597; MUID:75036120; PMID:4429673
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Sacession: S14711; A03113; A90597; S06555
R;Furet, J.P.; Mercier, J.C.; Soulier, S.; Gaye, P.; Hue-Delahaie, D.; Vilotte, J.L.
Nucleic Acids Res. 18, 5386, 1990
A;Title: Nucleotide sequence of ovine kappa-casein cDNA.
A;Reference number: S14711; MUID:90384837; PMID:2402453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 YQQKPVALINNQFLPYPYTAKPAVRSPAQILQWQVLSNTVPAKSCQAQPTTMARHPHPH 123
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A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Rossidues: 1-156, "I',158-168, "A',170-173, "T',175-190 <GO3>
A.Cross-references: GB:M36641; NID:g162810; PIDN:AAA30433.1; PID:g162811
C.Comment: The sequence shown is the A variant.
C.Genetics:
A.Introns: 19/3; 30/3
A.Introns: 19/3; 30/3
C.Superfamily: kappa-casein
C.Keywords: glycoprotein; milk; phosphoprotein
C.Keywords: glycoprotein; milk; phosphoprotein; phosphoprotein; milk; phosphoprotein; phosphoprotein; milk; phosphoprotein; milk; ph
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                                         ......e: Analysis of nucleotide sequence of bovine kappa-casein cdna.
A;Reference number: 145875
A;Gecssion: 145875
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44.4%; Pred. No. 3.4e-07;
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42.9%; Pred. No. 7.5e-07;
iive 6; Mismatches 22,
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                       R;Gorodetskii, S.I.; Kaledin, A.S.
Genetika 23, 398-404, 1987
A;Title: Analysis of nucleotide se
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Matches 27; Conservative
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A; Residues: 127-192 <JOL2>
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A; Residues: 22-101, 'D', 103-127 < MER>
A; Note: the amino-terminal residue appears to be pyrrolidone carboxylic acid, but cycliz
R; Grosclaude, F.; Mahe, M.F.; Mercier, J.C.; Ribadeau-Dumas, B.
Ann. Genet. Sel. Anim. 4, 515-521, 1972
A; Title: Localisation des substitutions d'acides amines differenciant les variants A et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 92-156, T. 158-168, A. 170-173, T. 175-190 <GO2>
A; Cross-references: GB:M3833; NID:g162806; PIDN:AAA30432.1; PID:g162807
A; Note: the authors translated the codon TrG for residue 100 as Pro and GAA for residue
Ex. J. Blochem. 35, 22-235, 1973
A; Title: Gructure primaire de la caseine kappaB bovine. Sequence complete.
A; Reference number: A91206; MUID:73216467; PMID:4577852
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A; Residues: 22, 70', 24-25, FE', 27, E', 29-126 < JO2>
B; Jolles, J: Schoentgen, F: Alais, C:; Fiat, A.M.; Jolles, P.
Helv. Chim. Acta 55, 2872-2883, 1972
A; Title: Studies on the primary structure of cow kappa-casein. Structural features of A; Reference number: A91634; MUID: 73124636; PMID: 4653404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title: Structure primaire du caseinomacropeptide de la caseine kappaB-1 bovine. Reference number: A60833; MUID:72254481; PMID:4559180
                                                                                                                                                                                                                                                                                                                                                                    A;Title: Primary structure of cDNA of Bos taurus kappa-casein macropeptide. A;Reference number: JN0364; MUID:85022828; PMID:6689612
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A;Title: Specificity of milk-clotting enzymes towards bovine kappa-casein. A;Reference number: S03993; MUID:89207571; PMID:2495817
A;Accession: S03993
A;Molecule type: protein
A;Residues: 126-130 <DRO>
A;Title: Analysis of nucleotide sequence of bovine kappa-casein cDNA.
                                                                                                                                                                                                                         A;Residues: 1-138,'G',140-156,'I',158-168,'A',170-173,'T',175-190
R;Gorodetsky, S.I.; Kershulite, D.D.; Korobko, B.G.
Bioorg. Khim. 9, 1693-1694, 1983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mercier, J.C.; Uro, J.; Ribadeau-Dumas, B.; Grosclaude, F.
nr. J. Biochem. 27, 535-547, 1972
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A; Residues: 128-156, 'I',158-168,'A',170-190 <ME2>
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Chimia 26, 645-646, 1972
A;Reference number: A90920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 128-190 <GRO>
A; Note: article in French with English abstract
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Residues: 127-156,'I',158-168;187-190 <GUE>
Experimental source: colostrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reference number: A90033
                                                                                            Contents: B2 variant; Accession: $06376
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Contents: B2 variant A; Accession: JN0364
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probable cell wall protein - garden pea
C; Species: Pisum sativum (garden pea)
C; Species: Pisum sativum (garden pea)
C; Date: 23.Apr.1999 #sequence_revision 23-Apr.1999 #text_change 20-Jun-2000
C; Accession: T06482
R; Bown, D.P.
Submitted to the EMBL Data Library, June 1992
A; Reference number: 21568
A; Reference number: 21568
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-352 < AGOWA
A; Residues: 1-352 < AGOWA
A; Residues: 1-352 < AGOWA
A; Cross-references: EMBL:X67427; PIDN:CAA47812.1
A; Experimental source: cv. Purple Podded
C; Genetics:
A; Gene: ptxA
C; Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rymechaler, S.L.; Nesburn, A.B.; Zwaagstra, J.; Ghiasi, H. Virology 168, 168-172, 1989
A/Title: Sequence of the latency-related gene of herpes simplex virus type 1. A; Reference number: A94388; MUID:89085598; PMID:2535901
A, Accession: A3337
A; Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell wall protein - alfaifa
C;Species: Medicago sativa (alfalfa)
C;Species: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jul-2000
C;Accession: S52885
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                                64 YQNRASVPINNPYLCHLYYVPSFVLWAQGQIPKGPVSTDIHQSTWQYHQAKHPSF 118
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A; Residues: 1-340 < WEC>
A; Cross-references: GB:J04323; NID:g330133; PIDN:AAA45799.1; PID:g330134
C; Genetics:
     1 YORRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF
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C;Superfamily: herpesvirus latency-related protein
C;Keywords: tandem repeat
F;26-41/Region: 16-residue tandem repeat
F;42-57/Region: 16-residue tandem repeat
F;58-73/Region: 16-residue tandem repeat
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llarity 37.3%; Pred. No. 0.71
Conservative 6; Mismatches
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Best Local Similarity
Matches 19; Conserv
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S52985
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A;Experimental Source: mammary gland
A;Bxperimental Source: mammary gland
B;Bosze, Z.Z.; Devinoy, E.E.; Puissant, C.C.; Fontaine, M.M.L.; Houdebine, L.L.M.
submitted to the EMBL Data Library, November 1992
A;Bestiption: Characterization of the rabbit kappa-casein cDNA: in vivo and in vitro
A;Reference number: S31623
A;Accession: S31623
                                                                                                                                                                                                   C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 13-Aug-1999
C; Accession: JC4955; S31623; S42802
R; Baranyi, M.; Aszodi, A.; Devinoy, E.; Fontaine, M.L.; Houdebine, L.M.; Boesze, Z. Gene 174, 27-34, 1996
A; Title: Structure of the rabbit kappa-casein encoding gene: Expression of the cloned A; Reference number: JC4955; MUID:97017124; PMID:8863725
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C;Species: cavia porcellus (guinea pig)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999
C;Accession: S12092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 55,'HT',58-165,'R',167 <DAW>
A;Cross-references: EMBL:X76910; NID:g439523; PIDN:CAA54232.1; PID:g439524
C;Genetics:
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A;Residues: 1-234 <HAL>
A;Cross:references: EMBL:X56020; NID:g49430; PIDN:CAA39497.1; PID:g49431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: EMBL:Z18243; NID:g1606; PIDN:CAA79145.1; PID:g1607
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A;Introns: 19/3; 30/3
C;Superfamily: Kappa-casein
C;Keywords: glycoprotein; mammary gland; milk; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.5%; Score 93; DB 2; Length 234 tharity 36.4%; Pred. No. 0.0029; Conservative 7; Mismatches 28; Indels
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Nucleic Acids Res. 18, 6129, 1990
A;Title: Nucleotide sequence of guinea-pig kappa-casein cDNA.
A;Reference number: S12092; MUID:91045081; PMID:2235497
A;Accession: S12092
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Pred. No. 2.5e-06;
7; Mismatches 22;
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submitted to the EMBL Data Library, December 1993
A:Reference number: $42802
A:Accession: $42802
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llarity 43.6%;
Conservative
                                                                                                                                                                                kappa-casein precursor - rabbit
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A; Residues: 1-180 <BAR>
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24; Conserv
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Molecule type: mRNA
Residues: 1-180 <BOS>
                                124 LSF 126
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PSF
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Best Local Simi
Matches 20;
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Best Local
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J. Biol. Chem. 258, 2911-2915, 1983
A; Title: Evidence for a repeating 3,4-dihydroxyphenylalanine- and hydroxyproline-cont A; Reference number: A20840; MUID:83135732; PMID:6298211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YORRPAIAINNPYVPRIYYANPAVVRPHAQIPQRQYLPN-----SHPPTV
            this peptide is the concensus tandem repeat decapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.3%; Score 65; DB 2; Length 875; 27.1%; Pred. No. 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 21.3%;
Best Local Similarity 37.5%;
Matches 24; Conservative
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Matches 19; Conservative
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152 KPKPSYPPSY 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: 226053
A; Accession: T52359
A; Status: preliminary
A; Molecule type: DNA
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C; Species: Nostoc sp. PCC 7120
A; Note: Nostoc sp. strain PCC 7120
A; Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C; Accession: AB2067
B; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, B. 785-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; WUID:21595285; PMID:11759840
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R;Deutch, C.E.; Winicov, I.
Plant Wol. Biol. 27, 411-418, 1995
A;Fitle: Post-transcriptional regulation of a salt-inducible alfalfa gene encoding A;Reference number: $52985; MUID:95195167; PMID:7888629
A;Recession: $52985
A;Status: preliminary
A;Wollcule type: DNA
A;Residues: 1-381 < DNA
A;Residues: 1-381 < DNA
A;Residues: 1-381 < DNA
A;Cross-references: EMBL:L37017; NID:93818415; PIDN:AAD03487.1; PID:93818416
C;Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1.875 <FIL>
A:Status: 1.875 <FIL>
A:Taylor, S.M.; Walte, J.H.; Ross, M.M.; Shabanowitz, J.; Hunt, D.F.
J. Am. Chem. Soc. 116, 10803-10804, 1994
A:Title: trans-2,3-cis-3,4-dihydroxyproline, a new naturally occurring amino acid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dolyphenolic adhesive protein 1 [validated] - blue mussel (fragment)
NAlternate names: MeFp-1
Cispecies: Mytilus edulis (blue mussel)
Cispecies: Aytilus edulis (blue mussel)
Cispate: 27-May-1994 #sequence_revision 10-Nov-1995 #text_change 02-Jun-2000
Cisaccession: S23760, A59158; A20840
RFilpula, D.R.; Lee, S.M.; Link, R.P.; Strausberg, S.L.; Strausberg, R.L.
Blottechnol. Prog. 6, 171-177, 1990
A;Title: Structural and functional repetition in a marine mussel adhesive protein.
A;Reference number; S23760; MUID:91025829; PMID:1367451
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Pred. No. 5.2;
6; Mismatches
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; Pred. No. 3.2;
10; Mismatches
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Best Local Similarity 42.19
Matches 16; Conservative
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Best Local Similarity
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Molecule type: DNA
Residues: 1-289 <KUR>
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hypothetical protein BilE6.80 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 20-0ct-2000 #sequence_revision 20-0ct-2000 #text_change 20-0ct-2000
C;Accession: T52359
R;Schulte, U.; Algn, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu submitted to the Protein Sequence Database, September 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QRRPAIAINNPYVPRTYYANPAV - VRPHAQI - - - - PQRQYLP - - - - NSHPPTVVR - RP 49
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
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A;Experimental source: BAC clone B11E6; strain OR74A
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Pred. No. 29;
5; Mismatches
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%; MCMURIABY, A. Submitted to the EMBL Data Library, May 1996
Submitted to the EMBL Data Library, May 1996
W; Reference number: 219977
W; Reference number: 219977
W; Status: preliminary; translated from GB/EMBL/DDBJ
W; Molecule type: DNA
W; Residues: 1-254 < WIL>
W; Cross-references: EMBL:273098; PIDN:CAA97336.1; GSPDB:GN00023; CESP:T21C9.9
W; Experimental source: clone T21C9
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YORRPAIAINNPYVPRIYYANPAVVRPHAQIPQROYLPNS-----HPPTVVRRPNL 51
                                                                                                                                                                                                                                                                                                                    Ouery Match 21.1%; Score 64.5; DB 2; Length 254;
Best Local Similarity 28.6%; Pred. No. 5.1;
Matches 18; Conservative 9; Mismatches 21; Indels 15; Gaps
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A;Gene: CESP:T21C9.9
A;Map position: 5
A;Introns: 22/2; 78/3
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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 11, 2003, 08:16:36 ; Search time 8.00971 Seconds (without allgoments) 322.917 Million cell updates/sec Run on:

US-09-508-095-17 305 1 YORRPAIAINNPYVPRTYYA.....VLPNSHPPTVVRRPNLHPSF 55 Title: Perfect score: . Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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No.	Score	Match	Score Match Length DB ID	DB	91	Description
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m	186	61.0		~	CASK BALPH	027055 balaenonto
4	183	60.09		-	CASK HORSE	D82187 AGIIIS OSES
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- 1	T/T	7.0C		4	CASK_HIPAM	028441 hippopotam

ption	homo santen	eduns	balaen	ednn	tapiro	uncia un	hippo		саше	tayassu	sus scro	buba	-	capricorn				nemorhaedu		bison	nrus	rupicapra r	ovis aries	cervus nipp	10	oryctolaqus	traqulus ja	qq	cervus unic		elaphurus d	odocoileus	en
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ID	CASK_HUMAN	CASK_EQUGR		CASK_HORSE	CASK_TAPIN	CASK_UNCUN	CASK_HIPAM	CASK_LAMGU	CASK_CAMDR	CASK_TAYTA	CASK_PIG	CASK_BUBBU	CASK_OREAM	CASK_CAPCR	CASK_CAPHI	CASK_CAPSU	CASK_CAPSW	CASK_NEMGO	CASK_SAITA	CASK_BISBO	CASK_BOVIN	CASK_RUPRU	CASK_SHEEP	CASK_CERNI	CASK_GIRCA	CASK_RABIT	CASK_TRAJA	CASK_CERDU	CASK_CERUN	CASK_OVIMO	- 1	- 1	CASK_ODOVI
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# ALIGNMENTS

RESULT 1

RA Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Bosak S.A., Moreyan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Pilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Willahom D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ra Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnutz J., Myers R.M., Schent J.B., Jonnes S.J.M., Marra M.A.;  R. Generation and initial analysis of more than 15,000 full-length	RL DNA Seq. 3:245-246(1992). RN [3] RP SEQUENCE FROM N.A. RX MEDLINE-97017129; PubMed-8863730; RA Edlund A., Johansson T., Leidvik B., Hansson L.; RT "Structure of the human kappa-casein gene."; RL Gone 174:65-69(1996). RN [4] RP SEQUENCE FROM N.A.	RP Menon R.S., Jeffers K.F., Chang Y.F., Ham R.G.; RL Submitted (XXX-1991) to the EMBL/GenBank/DDBJ databases. RL Submitted (XXX-1991) to the EMBL/GenBank/DDBJ databases. RN [2] RP SEQUENCE FROM N.A. RC TISSUE-Manmary gland; RX MEDLINE-93208373; PubMed-1296818; RA Bergstroem S., Hansson L., Hernell O., Loennerdal B., Nilsson A.K., RA Stroemqvist M.;	AC P07498; Q13575; DT 01-APR-1988 (Rel. 07, Created) DT 01-APR-1988 (Rel. 34, Last sequence update) DT 15-SEP-2003 (Rel. 42, Last annotation update) DE Kappa casein precursor. GN CSN3 OR CSN10 OR CSNK OR CASK. OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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20305 MW; 8A1609D2D5C94895 CRC64;

182 AA;

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                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@lsb-sib.ch).
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                                                                                                                                                         MEDLINE-99207197; PubMed-10191473; Plowman J.E., Creamer L.K., Liddell M.J., Cross J.J.; Plowman J.E., Creamer L.K., Liddell M.J., Cross J.J.; Structural features of a peptide corresponding to human kappa-casein residues 84-101 by 1H-nuclear magnetic resonance spectroscopy."; J. Dalry Res. 66:53-63(1999).
                                                                                                   Jolles
                                                                                                                                                                                                                              casein precipitation in milk.
SUBUNIT: HETEROMULTIMERS COMPOSED OF ALPHA-SI CASEIN AND KAPPA
CASEIN LINKED BY DISULFIDE BONDS.
SUBCELLULAR LOCATION: Extracellular.
TISSUE SPECIFICITY: MANMARY GIAND; MILK.
PTM: The N-terminus is blocked.
SIMILARITY: Balongs to the kappa-casein family.
DATABASE: NAME-Protein Spotlight;
NOTE-ISSUE 16 of November 2001;
WWW="http://www.expasy.org/spotlight/articles/sptlt016.html".
                                                                       CARBOHYDRATE-LINKAGE SITES, AND SEQUENCE OF 118-182.
MEDIINE-81114144; PubMed-7460900;
Fiat A.M., Jolles J., Aubert J.-P., Loucheux-Lefebvre M.H., Jolles
"Localisation and importance of the sugar part of human casein.";
Eur. J. Biochem. 111:333-339(1980).
SEQUENCE OF 25-182.
MEDLINE-82558132; Pubmed-4018271;
MEDLINE-81558132; Pubmed-4018271;
Blignon G., Chtourou A., Ribadeau-Dumas B.;
"Preparation and antino acid sequence of human kappa-casein.";
FEBS Lett. 188:48-54(1985).
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? -> C (IN REF. 4).

? -> L (IN REF. 3).

A -> T (IN REF. 1).

> -> N (IN REF. 5).
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InterPro; IPR000117; Casein_kappa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM: 601695; -. G. extracellular; NAS. 60: 60:0005576; C. extracellular; NAS. 60: 60:0007582; P:physiological proce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00997; casein_kappa; 1.
ProDom; PD003689; Casein_kappa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۲.
د
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X66417; CAA47048.1; -. U51899; AAC50772.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M73628; AAA59456.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U51899; AAC50772.1; -
EMBL; BC010935; AAH10935.1;
                                                                                                                                              STRUCTURE BY NMR OF 108-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR, JC4957; KKHU.
GlycoSuiteDB; P07498; -.
Genew; HGNC:2446; CSN3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SITE
CARBOHYD
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CARBOHYD
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                                                   Gaps
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                                                                                                                       63 YQRRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YORRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 55
                                                                                               1 YORRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 55
                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
CSN3 OR CSN10 OR CSNK.
CSN3 OR CSN10 OR CSNK.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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    Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.3%; Score 18/; ...
63.6%; Pred. No. 1.4e-14;
tive 4; Mismatches 16; Indels
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1EB97AE555F95402 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                casein precipitation in milk.
--- SUBCELLULAR LOCATION: Extracellular.
--- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
--- SIMILARITY: Belongs to the kappa-casein family.
Query Match
100.0%; Score 305; DB 1;
Best Local Similarity 100.0%; Pred. No. 8.5e-28;
Matches 55; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                135 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00997; casein_kappa; 1.
ProDom; PD003689; Casein_kappa; 1.
Milk; Phosphorylation; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000117; Casein_kappa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96364219; PubMed-8752004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 AA; 15221 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U53893; AAB08409.1; -
                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 61.3
Best Local Similarity 63.6
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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CSN3 OR CSN10 OR CSNK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CASK_BALPH
Q27952;
                                                                                                                                                                                                                                                              CASK_EQUGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
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SITE
                                                                                                                                                                                                               RESULT 2
CASK_EQUGR
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us-09-508-095-17.rsp

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Best Local Similarity
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Q29135;
                                                                                                                                                                                                                                                                         CONFLICT
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                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                     EMBL outstation
                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outstati
the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                   Gatesy J., Hayashi C., Cronin M.A., Arctander P.,
"Evidence from milk casein genes that cetaceans are close relatives
of hippopotamid artiodactyls."
Mol. Biol. Evol. 13:954-963(1996).
-I- FUNCTION: Kappa casein stabilizes micelle formation, preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YQRRPALAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- FUNCTION: Kappa casein stabilizes micelle formation, preventing
Balaenoptera physalus (Finback whale) (Common rorqual).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLEAVAGE (BY CHYMOSIN (=RENNIN))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 186; DB 1; Length 145;
Pred. No. 2e-14;
4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Lenasi T., Rogelj I., Dovc P.;
"Equus caballus Kappa-casein (k-CN) mRNA.";
Submitted (JUN-2001) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY);
17024F195EA78781 CRC64;
                                                                                                                                                                                            casein precipitation in milk.
-!- SUBCELCHAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
-!- SIMILARITY: Belongs to the kappa-casein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               casein precipitation in milk.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
-!- SIMILARITY: Belongs to the kappa-casein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tedeschi G.;
Submitted (NOV-1999) to the SWISS-PROT data bank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CASK_HORSE STANDARD; PRT; 185 AA. P82187, Q8SERD; CASK_HORSE STANDARD; PRT; 185 AA. P82187, Q8SERD STANDARD; PRT; 185 AA. 15-SEP-2003 (Rel. 42, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) CSN3.OR CSN10.
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000117; Casein_kappa.
Pfam: PF00997; casein_kappa; 1.
Probom; PD003689; Casein_kappa; 1.
MILK: Phosphorylation; Glycoprotein.
NON_TER
                                                                                         SEQUENCE FROM N.A.
MEDLINE-96364219; PubMed-8752004;
                                               Balaenopteridae; Balaenoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16324 MW;
                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U53888; AAB08404.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 61.8%;
les 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 21-181.
                                                                NCBI_TaxID=9770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FISSUE-Milk;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CASK_HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-96364219; PubMed-8752004; MEDLINE-96364219; PubMed-8752004; Gatesy J., Haysahi C., Croin M.A., Arctander P.; Bridence from milk casein genes that cetaceans are close relatives of hippopotamid artiodactyls."; Mal. Biol. Evol. 13:954-963[1996].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YQRRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tapirus indicus (Asiatic tapir) (Malayan tapir).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Perissodactyla, Tapiridae, Tapirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                               KAPPA CASEIN.
CLEAVAGE (BY CHYMOSIN (-RENNIN))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLEAVAGE (BY CHYMOSIN (*RENNIN))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 183; DB 1; Length 185;
Pred. No. 5.7e-14;
4; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
TCHKND -> RCVKNH (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                     -> VV (IN REF. 2).
F7634F52CEE90606 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the kappa-casein family.
                                                                                                                                                                                                                                                                                                                                                                                  C -> R (IN REF. 2)
V -> VV (IN REF. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    casein precipitation in milk.
--- SUBCELLULAR LOCATION: Extracellular.
--- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U53892; AAB08418.1; -.
InterPro; IPR000117; Casein_kappa.
Pfam; PP00997; Casein_kappa.
ProDom; P0003689; Casein_kappa; 1.
Milk; Phosphorylation; Glycoprotein.
NON_TER
80 81 CLEAVAGE
                                                                                                                                                                   EMBL; AY040863; AAK83669.1; -.
InterPro; IPR000117; Casein_kappa.
Prodom; PF00997; Casein_kappa; 1.
Prodom; PD003689; Casein_kappa; 1.
Milk; Phosphorylation; Signal.
                                                                                                                                                                                                                                                                                                                                                          34 TC
112 C
152 V
21021 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kappa casein (Fragment).
CSN3 OR CSN10 OR CSNK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                               185
118
                                                                                                                                                                                                                                                                                                                                                          29
112
152
185 AA;
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Matches

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                                                                                                                     Gatesy J., Hayash C., Cronin M.A., Arctander P.;
"Evidence from milk casein genes that cetaceans are close relatives of hippopotamid articodactyls.";
Mol. Blol. Evol. 13:954-953(195);
-i- FUNCTION: Kappa casein stabilizes micelle formation, preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YQRRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eutheria, Cetartiodactyla, Hippopotamidae, Hippopotamus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lama guanicoe (Guanaco).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 91 N-LINKED (GLCNAC. .) (POTENTIAL).
145 AA; 16272 MW; 874A9EEFD6F80398 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Indels
                                                                                                                                                                                                                       casein precipitation in milk.
--- SUBCELLULAR LOCATION: Extracellular.
--- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
--- SIMILARITY: Belongs to the kappa-casein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.1%; Score 171; DB 1;
60.0%; Pred. No. 1e-12;
11ve 5; Mismatches 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00997; casein kappa; 1.
ProDom; PD003689; Casein kappa; 1.
Milk; Phosphorylation; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000117; Casein_kappa.
                                                                                                        MEDLINE-96364219; PubMed-8752004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U53889; AAB08413.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.0
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kappa casein (Fragment).
CSN3 OR CSN10 OR CSNK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                              NCBI_TaxID=9833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CASK_LAMGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
CASK_LAMGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   028451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-96364219; PubMed-8752004; MEDLINE-96364219; PubMed-8752004; Gatesy J., Hayashi C., Cronin M.A., Arctander P.; Gatesy J., Hayashi C., Cronin M.A., Arctander P.; Evidence from milk casein genes that cetaceans are close relatives of hippopotamid artiodactyls."; Mol. Biol. Evol. 13:954-963(1996).

1- FUNCTION: Kappa casein stabilizes micelle formation, preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                               1 YQRRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 55
                                                                                                                                                     1 YQRRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 55
                                                                                                                                                                                                                                                                                                                                                                                               Uncia uncia (Snow leopard) (Panthera uncia).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Uncia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                              Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 181; DB 1; Length 146;
Pred. No. 7.4e-14;
                                                        Score 181; DB 1; Length 14
Pred. No. 7.4e-14;
3; Mismatches 18; Indels
Y SIMILARITY).
E8957001E0AB59CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 AA; 16337 MW; D667EDEF607E5E66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 casein precipitation in milk.
--- SUBCELLULAR LOCATION: Extracellular.
--- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
--- SIMILARITY: Belongs to the kappa-casein family.
                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
CSN3 OR CSN10 OR CSNK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                          146 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylation; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000117; Casein_kappa.
Pfam; PF00997; casein_kappa; 1.
ProDom; PD003689; Casein_kappa; 1.
  (BY
                  16691 MW;
                                                        59.3%;
61.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.3%;
58.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U53894; AAB08421.1; -.
                                                                      Best Local Similarity 61.8
Matches 34; Conservative
                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kappa casein (Fragment).
CSN3 OR CSN10 OR CSNK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                  146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-29064;
                                                                                                                                                                                                                                                                CASK_UNCUN
Q29150;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CASK_HIPAM
Q28441;
01-NOV-1997 (
01-NOV-1997 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-SEP-2003
                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Hippopotamus amphibius (Hippopotamus).

Loca 1

CASK\_HIPAM

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Length 145;

Euteleostom1;

STEFF

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    63 YQHRLAVPINNQFIPYPNYAKPVAIRLHAQIPQCQALPNIDPPTVERRPRPRFSF 117
                                                                                                                                                                                                                                                                                                                           1 YQRRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                        Kappa casein (Fragment).
CSN3 OR CSN10 OR CSNK.
Tayassu tajacu (Collared peccary) (Pecari tajacu).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
Mammalia; Eutheria; Cetartiodactyla; Suina; Tayassuidae; Pecari.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLEAVAGE (BY CHYMOSIN (-RENNIN))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY).
133188256EC2C038 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the kappa-casein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 160; DB 1;
Pred. No. 1.8e-11;
                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Kappa casein precursor
CSN3 OR CSN10 OR CSNK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
                                                                                                    146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Pred. No. 1.86
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD003689; Casein_kappa; 1.
Milk; Phosphorylation; Glycoprotein.
                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000117; Casein_kappa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      700997; casein_kappa; 1.
PD003689; Casein_kappa; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Mammary gland;
MEDLINE=92367959; PubMed=1503275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1989 (Rel. 12, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 AA; 16405 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.5%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U53891; AAB08416.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                        NCBI_TaxID=9829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00997
                                                                                                  CASK_TAYTA
Q28794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P11841;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CASK_PIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
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requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          **Rappeler S., Farah Z., Pubna Z.;

"Sequence analysis of Camelus dromedarius milk caseins.";

"Sequence analysis of Camelus dromedarius milk caseins.";

J. Dalry Res. 65:209-222(1998).

-! FUNCTION: Kappa casein stabilizes micelle formation, preventing casein precipitation in milk.

-! SUBCELLULAR LOCATION: Extracellular.

-! TISSUE SPECIFICITY: MAMMARY GLAND; MILK.

-! SIMILARITY: Belongs to the kappa-casein family.
                                                                                                                                                                                                                                                                                                                           1 YORRPAIAINNPYVPRIYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 55
                                                                                                                                                                                                                                                                                                                                               1 YORRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelidae, Camelus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAPPA CASEIN.
CLEAVAGE (BY CHYMOSIN (-RENNIN)) (BY.
SIMILARITY).
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                                                                                                                                                                    CLEAVAGE (BY CHYMOSIN (-RENNIN))
                                                                                                                                                                                                                                                Score 165; DB 1; Length 125; Pred. No. 4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Indels
                                                                                                                                                                                                          9E51E7A07EC8400B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            418D19E061DA7338 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSN3 OR CSN10 OR CSNK.
Camelus dromedarius (Dromedary) (Arabian camel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 165; DB 1;
Pred. No. 6.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-SEP-2003 (Rel. 42, Last annotation update)
Kappá casein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR000117; Casein_kappa.
Pfam; PF00997; casein_kappa; 1.
ProDom; PD003689; Casein_kappa; 1.
Milk; Phosphorylation; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 AA
                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                      InterPro; IPR000117; Casein_kappa.
Pfam; PF00997; casein_kappa; 1.
ProDom; P0003689; Casein_kappa; 1.
Milk; Phosphorylation; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Somall; TISSUE-Udder;
MEDLINE-98291310; PubMed-9627840;
                                                                                                                                                                                          (BY
                                                                                                                                                                                                          125 AA; 13795 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20417 MW;
                                                                                                                                                                                                                                                54.18;
58.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.1%;
58.2%;
                                                      EMBL; U53890; AAB08415.1; -.
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                                                                                                                                                                                                                                                                Best Local Similarity 58.2
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                    29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CASK_CAMDR
P79139;
                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                              Query Match
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CASK_OREAM
                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P50423;
                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                                                                                   SITE
   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                  Kappa caseins.;
FEBS Lett. 72:173-178(1976).

FEBS Lett. 72:173-178(1976).

FEBS Lett. 72:173-178(1976).

FUNCTION: Kappa casein stabilizes micelle formation, preventing casein precipitation in milk.

FUNCTION: Extracellular.

FUNCTION: MAMMARY GLAND; MILK.

FUNCTION: Belongs to the Kappa-casein family.

SIMILARITY: Belongs to the Kappa-casein family.
                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bloinformatics and the EMBL outstation. the European Bloinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YQRRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF 55
                                                                    MEDLINE-77068846; PubMed-1001463; Chobert J.M., Mercier J.-C., Bahy C., Haze G.; Primary structure of the casein macropeptide of porcine and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CASK_BUBBU STANDARD, PRT, 190 AA.
P11840.
01-0CT-1989 (Rel. 12, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 62, Last annotation update)
CSN3 OR CSN10 OR CSNK.
Bubalus bubalis (Domestic water buffalo).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Primary structure of the casein macropeptide of kappa casein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.
MEDLINE-96139018; PubMed=8587130;
Chikuni K., Moni Y., Tabata T., Saito M., Monma M., Kosugiyama
Chikuni K., Mori Y., Tabata T., Saito M., Monma M., Kosugiyama
"Molecular phylogeny based on the kappa-casein and cytochrome b
sequences in the mammalian suborder Ruminantia.";
J., Mol. Evol. 41:859-866(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLEAVAGE (BY CHYMOSIN (=RENNIN))
Levine W.B., Alexander L.J., Hoganson G.E., Beattle C.W.; "Cloning and sequencing of the porcine kappa-casein cDNA."; Anim. Genet. 23:361-363(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.5%; Score 160; DB 1; Length 188; illarity 54.5%; Pred. No. 2.3e-11; Conservative 5; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3Y SIMILARITY).
9B41E4BE19B5D36A CRC64;
                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR000117; Casein_kappa.
Pfam; PF00997; casein_kappa; 1.
ProDom; PD003689; Casein_kappa; 1.
Milk; Glycoprotein; Phosphorylation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
KAPPA CASEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-7722193; PubMed-328059;
Addeo F., Mercier J.-C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21122 MW;
                                                                                                                                                                                                                                                                                                                                              EMBL; X51977; CAA36239.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochimie 59:375-379(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovidae; Bovinae; Bubalus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 116-190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=89462;
                                                                                                                 kappa caseins.
                                                         SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                              PIR; A48382;
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Best Local S:
Matches 30,
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                                                                                                                                                                                                                   noved. Usage by and for commercial
(See http://www.lsb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 YQQKPVALINNQFLPYPYYAKPAAVRSPAQILQWQVLPNTVPAKSCQAQPTTMTRHPHPH 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE OF 69-192 FROM N.A.
MEDLINE-37055443; PubMed-8899730;
CTOMIA M.A., Stuart R., Pierson B.J., Patton J.C.;
"K-casein gene phylogeny of higher ruminants (Pecora, Artiodactyla).";
Mol. Phylogenet. Evol. 6:295-311(1996).
-1- FUNCTION: Kappa casein stabilizes micelle formation, preventing
casein precipitation in milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YQRRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPN-----SHPPTVVRRPNLH
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-1-.FUNCTION: Kappa casein stabilizes micelle formation, preventing casein precipitation in milk.
--- SUBCELLULAR LOCATION: Extracellular.
--- TISSUE SPECIFICITY: MANMARY GLAND; MILK.
--- SIMILARITY: Belongs to the kappa-casein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=96139018; PubMed=8587130;
Chikuni K., Moril Y., Tabata T., Saito M., Monma M., Kosugiyama M.;
"Molecular phylogeny based on the kappa-casein and cytochrome b sequences in the mammallan suborder Ruminantia.";
J. Mol. Evol. 41:859-866(1995).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLEAVAGE (BY CHYMOSIN (-RENNIN))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 190;
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Pred. No. 1.6e-08;
7; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
O-LINKED (GALNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Signal.
BY SIMILARITY.
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                                                                                                                                                                                                                                          entities requires a license agreement (Se or send an email to license@isb-sib.ch).
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EMBL; D14368; BAA03285.1; JOINED.
EMBL; D14369; BAA03285.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD003689; Casein_kappa; 1
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CSN3 OR CSN10 OR CSNK.
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190
127
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Best Local Similarity
Matches 29; Conserv
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Pfam; PF00997;
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(Goat).
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CASK_CAPHI
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DDT AC
                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@labs.sib.ch).
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PHOSPHOKYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
95BA346766DD402A CRC64;
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Boyldae; Caprinae; Capricornis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 192;
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             -:- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 134; DB 1;
Pred. No. 2.1e-08;
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01-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                       Probom; PD003689; Casein_Fappa; 1.
Milk; Phosphorylation; Glycoprotein; Signal;
Pyrrolidone carboxylic acid. BY SIMILARITOV
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                                                                                                                                                                                                                                                                                                                                                                                                     KAPPA CASEIN
SUBCELLULAR LOCATION: Extracellular.
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EMBL; D32184; BAA06886.1; JOINED.
EMBL; U37512; AAC48658.1; -
                                                                                                                                                                                                                                                                                     InterPro; IPR000117; Casein_kappa.
Pfam; PF00997; casein_kappa; 1.
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CSN3 OR CSN10 OR CSNK,
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172
189
192 AA;
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P42156;
01-NOV-1995 (
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MOD_RES
SEQUENCE
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to licensee@isb-sib.ch).
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
NCBI_TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CASK_CAPHI STANDARD; PRT; 192 AA.
PO2670; Q8SPM9; Q8SPN0; Q8SPW6; Q8SPW7; Q8SPW8; Q8WMV5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLEAVAGE (BY CHYMOSIN (*RENNIN)) (BY SIMILARITY).
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MEDLINE=94042560; PubMed-8226388;
Coll A., Folch J.M., Sanchez A.;
"Nucleotide sequence of the goat kappa-casein cDNA.";
J. Anim. Sci. 71:2833-2833(1993);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 129; DB 1;
Pred. No. 7.8e-08;
6; Mismatches 21;
                                                                                                                                                                                                                       EMBL; D14374; BAA03287.1; JOINED.
EMBL; D14375; BAA03287.1; JOINED.
INTERPROPOSTOR CASEID. Kappa.
Pfam: PF00997; casein. Kappa. 1.
ProDom; PD003689; Casein. Kappa: 1.
MAILK; Phosphorylation: Glycoprotein; Signal;
Pyrrolidone carboxylic acid.
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01-AUG-1992 (Rel. 23, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Kappa caseth precursor (Kappa-CN).
CSN3 OR CSNNO OR CSNK.
                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAPPA CASEIN.
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Mercier J.-C., Addeo F., Pelissier J.-P.;
Unpublished results, cited by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
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172
189
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Best Local Similarity
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ProDom; PD003689; Casein\_kappa; 1.
Milk; Phosphorylation; Glycoprotein; Signal; Polymorphism;
Pyrrolidone carboxylic acid.

SIGNAL

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                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 31-192 FROM N.A., AND VARIANTS ARG-65; ILE-86; ILE-140 AND
                                              SEQUENCE OF 31-192 FROM N.A., AND VARIANTS ARG-65; ILE-86; ILE-140 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 31-189 FROM N.A., AND VARIANT ILE-140.
Fellgini M., Cubric-Curik V., Parma P., Curik I., Greppi G., Enne G.;
"Polymorphism of kappa-casein in Italian goat breeds: a new ACRS-PCR designed DNA test for discrimination of A and B alleles.";
Food Technol. Biotechnol. 40:293-298(2002).
                                                                                             Caroli A., Jann O., Budelli E., Bolla P., Jaeger S., Erhardt G.; "Genetic polymorphism of goat kappa-casein (CSN3) in different breeds and characterization at Davel."; Anim. Genet. 32:226-230(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Kappa casein stabilizes micelle formation, preventing
                                                                                                                                                                            SEQUENCE OF 31-192 FROM N.A., AND VARIANTS ILE-86; ILE-140; VAL-177
                                                                                                                                                                                                                                                                                    SEQUENCE OF 31-192 FROM N.A., AND VARIANTS GLY-111 AND LLE-140. Angiolillo A., Yahyaoui M.H., Sanchez A., Pilla F., Folch J.M.; "Characterization of a new genetic variant in the caprine k-casein
                                                                                                                                                                                                                                                                                                                                                                                                                                    Characterization of new genetic variants and genotyping of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDDINE-7711269; PubMed-1016651;
Mercier J.-C., Addeo F., Pelissier J.-P.;
"Primary structure of the casein macropeptide of caprine kappa
                                                                                                                                                                                                                        kahyaoui M.H., Coll A., Sanchez A., Folch J.M.;
"Genetic polymorphism of the caprine kappa casein gene.";
J. Dairy Res. 68:209-216(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   caprine kappa casein gene.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       casein precipitation in milk.
--- SUBCELLULAR LOCATION: Extracellular.
--- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
--- SIMILARITY: Belongs to the kappa-casein family.
Mercier J.-C., Chobert J.-M., Addeo F.; FEBS Lett. 72:208-214(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                     Tahyaoui M.H., Sanchez A., Folch J.M.;
                                                                                                                                                                                                        MEDLINE-21395138; PubMed-11504385;
                                                                                MEDLINE-21422902; PubMed-11531704;
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D14372; BAA03286.1; JOINED.
X60763; CAA43174.1; -
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AF485339; AAL90871.1;
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PR000117; Casein\_kappa

nterPro;

Pfam; PF00997; casein\_kappa;

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64 YQQRPVALINNQFLPYPYYAKPVAVRSPAQTLQWQVLPNTVPAKSCQDQPTTLARHPHPH 123
                                                                                                                                                                                                                                                                                                       1 YORRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNS------HPPTVVRRPNLH
                                                                              Q -> R (in allele CSN3-B).
V -> I (in alleles CSN3-B, C and G).
D -> G (in allele E).
V -> I (in allele E).
allele C, allele E, allele F and allele
                                                                                                                                                                                                                                                                           Gaps

G).
A -> V (in allele C).
S -> P (in alleles CSN3-B, C, F and G)
D -> N (IN REF. 3).
009F5858F4BFB178 CRC64;

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                          CLEAVAGE (BY CHYMOSIN (-RENNIN)).
PYRROLIDONE CARBOXYLIC ACID.
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Pred. No. 7.8e-08;
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6; Mismatches
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Best Local Similarity 44,4%;
Matches 28; Conservative
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192 AA;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Ailūrus fulgens (Lesser panda). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Carnivora, Fissipedia, Procyonidae, Ailurus. Gatesy J.;
"More DNA support for a Cetacea/Hippopotamidae clade: the blood .. 0 Query Match
71.5%; Score 218; DB 6; Length 146;
Best Local Similarity 69.1%; Pred. No. 3.5e-19;
Matches 38; Conservative 6; Mismatches 11; Indels NON\_TER 1 1 1 SEQUENCE 146 AA; 16478 MW; 069878C81C0CAB45 CRC64; 01-MAY-1997 (TrEMBLrel. 03, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) clotting protein gene g-fibrinogen.
Mol. Biol. Evol. 0:0-0(1997).
EMBL, U86645, AAB47431.1; -.
InterPro. IPR000117; Casein\_kappa.
ProDom; PD003689; Casein\_kappa; 1. Kappa casein (Fragment) SEQUENCE FROM N.A. NCBI\_TaxID=9649; 

1 YORRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNSHPPTVVRRPNLHPSF RESULT 2

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145 AA

Q28354 PRELIMINARY; PRT; Q28354; 01-NOV-1996 (TrEMBLrel. 01, Created)

028354 ID 0 AC 0 DT 0

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Kappa casein.
Equus caballus (Horse).
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Mammalia, Eutheria, Cetartiodactyla, Cetacea, Odontoceti, Delphinidae,
unidentified Delphinidae.
                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-96364219; PubMed-8752004;
Gatesy J., Hayashi C., Cronin M.A., Arctander P.;.
"Evidence from milk casein genes that cetaceans are close relatives of hippopotamid artiodactyls.";
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Physeler catcon (Sperm whale) (Physeter macrocephalus).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Physeteridae; Detartiodactyla; Cetacea; Odontoceti;
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More DNA support for a Cetacea/Hippopotamidae clade: the blood
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Mol. Biol. Evol. 0:0-0(1997).
EMBL, U86643; AAB47429.1; -.
InterPro; IPR000117; Casein_kappa.
ProDom; PD003689; Casein_kappa; 1.
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EMBL; U53887; AAB08407.1; -.
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ProDom; PD003689; Casein_kappa; 1.
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60.0%;
01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19, K-casein (Fragment).
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                Delphinidae gen. sp.
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                                                                                                                                                   NCBI_TaxID=49273
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SEQUENCE
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1 YQRRPAIAINNPYVPRIYYANPAVVRPHAQIPQRQYLPNS------HPPTVVRRP 49.
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Connochaetes gnou (black wildebeest).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
     Euteleostom1;
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Matchec C.A., Davis S.K.,
Matthec C.A., Davis S.K.,
"Molecular Insights into the Evolution of the Family Bovidae: A
Nuclear DNA Perspective.";
Nuclear DNA Perspective.";
Nuclear DNA Perspective.";
Interpro, 1811220-1230(2001).
EMBL; AF210161; AAK6779 1:
Interpro, IPR000117; Casein_kappa.
Pfam: PP00997; casein_kappa.
ProDom; PD003689; Casein_kappa; 1.
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                                                                                                                     Lenasi T., Rogelj I., Dovc P.;
"Equus caballus kappa-casein (k-CN) mRNA.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY040863; AAR83669.1;
InterPro: IPR000117; Casein_kappa.
Pfam; PF00997; casein_kappa:
Probom; PD003889; casein_kappa; J.
SEQUENCE: 185 AA; 21021 MW; F7634F52CEE90606 CRC64;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Last annotation update)
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Pred. No. 1e-08;
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Best Local Similarity 47.4 Matches 27; Conservative
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Capra hircus (Goat).
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1 YORRPAIAINNPYVPRTYYANPAVVRPHAQIPQRQYLPNS------HPPTVVRRPNLH 52
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
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Capra hirous (Goat).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Caprinae; Capra.
                                                                                                                                                                                                     SEQUENCE FROM N.A.
Yahyaoui M.H., Sanchez A., Folch J.M.;
Yahyaoui M.H., Sanchez A., Folch J.M.;
Characterization of new genetic variants and genotyping of the caprine kappa casein gene.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY090466; AMM12026.1;
InterPro; IRFR00117; Casein_Kappa.
InterPro; IRFR00117; Casein_Kappa.
Probon; P0003689; Casein_Kappa; 1.
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42.3%; Score 129; DB 6; Length 162;
Best Local Similarity 44.4%; Pred. No. 3.5e-08;
Matches 28; Conservative 6; Mismatches 21; Indels
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Yahyaoul M.H., Coll A., Sanchez A., Folch J.M.;
"Genetic polymorphism of the caprine kappa casein gene.";
J. Dairy Res. 68:209-216(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yahyaoui M.H., Coll A., Sanchez A., Folch J.M.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, A4485340; AAL9087.1; -.
Interpro; IFR00117; Casein_Kappa.
Pfam; PF00997; casein_Kappa. 1.
ProDom; PD0003689; Casein_Kappa; 1.
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SEQUENCE 162 AA; 18065 MW; 17D460D41923C77E CRC64;
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Last sequence update)
Last annotation update)
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Pred. No. 3.5e-08;
6; Mismatches 21;
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   01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-OCT-2002 (TrEMBLrel. 22,
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Best Local Similarity 44.4%;
Matches 28; Conservative
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                                                          Kappa casein (Fragment).
KAPPA CASEIN.
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Food Technol. Biotechnol. 0:0-0(2002).
EMBL, AF4348F; AL31534.1;
InterPro; IPR00117; Casein_kappa.
Prodom: PD003689; Casein_kappa. 1.
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Food Technol. Bio. 0:00-0(2002).

EMBL: AF434988; AA131535.1; -

InterPro: IPR00017; Casein_kappa.

ProDom: PD003689; Casein_kappa: 1.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                                                                                                   Length 159;
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42.3%; Score 129; DB 6; Length 155
Best Local Similarity 44.4%; Pred. No. 3.4e-08;
Matches 28; Conservative 6; Mismatches 21; Indels
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44.4%; Pred. No. 3.4e-08;
1ve 6; Mismatches 21; Indels
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159 AA; 17736 MW; 441923C77E4FEBAB CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Bovidae; Caprinae; Capra
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Capra hircus (Goat).
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Best Local Similarity
Matches 28; Conserv
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162 AA; 18007 MW; 17D60F298B4C3AEE CRC64;
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Capra hircus (Goat).
                                   Query Match
Best Local Similarity
Local 28; Conserve
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SEQUENCE FROM N.A.
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NON_TER
SEQUENCE
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08SPM9
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                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Yahyaoui M.H., Coll A., Folch J.M., Sanchez A.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF485399; AAL99871.1;
InterPro; IFR000117; Casein, Kappa.
Pfam; PF00997; casein_kappa; 1.
ProDom; PD003689; Casein_kappa; 1.
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Last annotation update)
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Last sequence update)
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                                                                                                                                                        162 AA.
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InterPro; IPR000117; Casein_kappa.
Pfam; PF00997; casein_kappa; 1.
ProDom; PD003689; Casein_kappa; 1.
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01-000-2002 (TrEMBLrel. 21, La
01-0CT-2002 (TrEMBLrel. 22, La
Kappa casein (Fragment).
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                                                                                                                                                                                                                                                                                                                                    Bovidae; Caprinae; Capra.
                                                                                                                                                      PRELIMINARY;
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Best Local Similarity
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              55
                                                    LSF 96
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              PSF
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Q8SPW8
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Q8SPV1
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last sequence update)
(1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Kappa casein (Fragment).
KAPPA CASEIN.
Capra hircus (Goat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Coprines; Caprines; Capra.
MCBI_TaxID=9925;
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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"Characterization of new genetic variants and genotyping of captine kappa casein gene.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY090467; AAM12027.1; -
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  Length 162;
                                                      21; Indels
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Last annotation update)
Score 129; DB 6;
Pred. No. 3.5e-08;
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Yahyaoui M.H., Coll A., Sanchez A., Folch J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                  162 AA
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                                                      6; Mismatches
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Search completed: August 11, 2003, 08:20:51
Job time : 34.0388 secs
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94 LSF 96
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fan B., L1 N., Wu C.;
"Research on the Sequences of Milk Protein Genes in Ruminants.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF194089; AAF63191.1;
InterPro; IPR000117; Casein_kappa.
Probom: PF00997; Casein_kappa.
Probom: PD03689; Casein_kappa; 1.
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44.4%; Pred. No. 6e-08;
Live 7; Mismatches 20; Indels
                                                                                                                                                                    Length 162;
"Genetic polymorphism of the caprine kappa casein gene.";
J. Dairy Res. 68:209-216(2001).
[2]
                                                                                                                                                                 / Match 42.0%; Score 128; DB 6; Length 16 Local Similarity 44.4%; Pred. No. 4.6e-08; nes 28; Conservative 6; Mismatches 21; Indels
                                           SEQUENCE FROM N.A.
Yahyaoui M.H., Coll A., Sanchez A., Folch J.M.;
Yahyaoui M.H., Coll A., Sanchez A., Folch J.M.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF465341; AAL90873.1.
InterPro; IFR000117; Casein_kappa.
Pfam; PF00997; casein_kappa.
ProDom; PD003689; Casein_kappa; 1.
                                                                                                                                           162 AA; 18117 MW; ECF5A9E590C465E6 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 21, Last annotation update)
Kappa-casein (Fragment).
Bos mutus grunniens (Yak)
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Last annotation update)
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Matches 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=30521;
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34 YQOKPVALINNQFLPYPYYAKPAAVRSPAQILQWQVLSNTVPAKSCQAQPTTWARHPHPH 93
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STRAIN-Sahiwal x Friesian;
MEDLINE-99304601; PubMed=10376313;
Prinzenberg E.M., Erhardt G.;
"A new CSN3 allele in Bos indicus cattle is characterised by MspI PCR-RFLP.";
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                                                                                                                                                                                                                                       STRAIN=Sahiwal x Friesian;
MEDLINE=20118591, PubMed=10654430;
MEDLINE=20118591, PubMed=10654430;

"SSCP analysis at the bovine CSN3 locus discriminates six alleles corresponding to known protein variants (A, B, C, E, F, G) and three new DNA polymorphisms (H, I, Al).";
Anim. Biotechnol. 10:49-62(1999).
Bos indicus x Bos taurus (hybrid cattle).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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SEQUENCE 160 AA; 17879 MW; F9A17987D81EF783 CRC64;
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InterPro; IPR000117; Casein kappa.
Pfam; PF00997; casein kappa; 1.
Probom; PD003689; Casein kappa; 1.
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                                                                                            Bovidae; Bovinae; Bos.
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Run on:

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Bifidobacterium bifidus stimulating peptide 19.
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                                                                          AAR22423
AAY31152
AAR22424
AAY31153
AAR45199
AAR45198
 AAY58733
AAG77906
AAB97382
AAE28002
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AAB36843
AAG77909
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AAB22822
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AAW71180
AAW21695
AAW53879
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AAB36842
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AAR43653
AAW09342
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AAE02341
AAW10519
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AAW86021
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   (first entry)
                                            Bifidobacterium bifidus
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AAW93883;
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                                                                                                               (without alignments)
217.984 Million cell updates/sec
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SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
SIDSI/gcgdata/geneseqy-embl/AA1990.DAT:*
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                                                                                            August 11, 2003, 08:16:37 ; Search time 34.9515 Seconds
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           5.1.6
Compugen Ltd.
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           GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
                                                                  OM protein .- protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Mutant human lacto Human lactoferrin Human lactoferrin Human lactoferrin Frotein encoded by Human lactoferrin Lactoferrin.

Bovine alphas1-cas Human lactoferrin Human lactoferrin

Chronic hepatitis

Human lactoferrin. Human lactoferrin. Human lactoferrin.

Human lactoferrin Human lactoferrin Human lactoferrin

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lactoferrin lactoferrin

Human lactoferrin Human lactoferrin Lactoferrin 6 kD v

Lactoferrin 6 kD v Bifidobacterium bi

Lactoferrin 6 kD v Lactoferrin 6 kD v

Amino acid sequenc Human lactoferrin Lactoferrin derive Antifungal peptide

Human lactoferrin. Human lactoferrin. Human lactoferrin

Bifidogenic peptide; protease; treatment; microbe-related disease; bacteria; fungi; yeast; protozoa; virus; mycoplasma; filaria; plasmodia; infection; inflammation; microbial induced tumour; degenerative disorder; diarrhoea; colic; oral microflora; intestinal microflora; caries; Location/Qualifiers 98DE-1005385 97DE-1040604 98WO-EP05899 (FORS/) FORSSMANN W. Key Disulfide-bond Disulfide-bond 11-FEB-1998; 16-SEP-1997; WO9914231-A2 16-SEP-1998; 25-MAR-1999 NAME OF THE PROPERTY OF THE PR

Bifidobacterium bi Bifidobacterium bi Human lactoferrin Human lactoferrin Lactoferrin decomp

Description

Amino acid sequenc Human lactoferrin Human codon optimi Codon optimised la

AAW93884
AAB22817
AAR87906
AAR91192
AAR8218
AAG77908
AAE27884

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48 49 51 52 52 54 690 690

261 261 261 261 261 261 261

AAW93883

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Result ٠ يو Zucht H;

Liepke C,

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treatment for 2 hr with proteases, then centrifuging to remove fat and cardifying to pH 2 to precipitate proteins. The solution phase is then subjected to reverse-phase high-performance liquid chromatography (HPLC) and cation-exchange HPLC, the fractions adjusted to salt content below growing Bifidobacterium bifidus and tested for activity by growing Bifidobacterium bifidus and Escherichia coli in presence of the fractions. Those fractions for which (Bw-BO) - (Ew-EO) is at least 0.15 fractions. Those fractions for which (Bw-BO) - (Ew-EO) is at least 0.15 see selected where Bw - germ count after 16 hr culture of B. Diffidus in 50% Elliker broth containing peptide at 0.2 mg/ml, BO - germ count under similar conditions in a peptide-free control, Ew = germ count after 16 hr culture of E. coli in 3 yl tryptic broth containing peptide at 0.2 mg/ml, BO - garm count under 0.2 mg/ml, BO - garm count under similar conditions in a peptide-free control. The peptide free fat control. The peptide fat control. The fat microbe-related
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infection; inflammation; microbial induced tumour; degenerative disorder;
diarrhoea; colic; oral microflora; intestinal microflora; caries;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diseases caused by bacteria, fungi, yeast, protozoa, viruses, mycoplasma, filaria and plasmodia, e.g. infections, inflammation, microbially induced tumours or degenerative disorders, diarrhoea, colic, abnormalities in oral, intestinal or vaginal microflora, or caries.
                                                                                                                                                                                           This invention describes milk-derived bifidogenic peptides and their active derivatives or fragments, and combinations of them produced by chemical coupling. Such are produced from bovine or human milk by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease;
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                                                                                                             Milk-derived peptides that stimulate Bifidobacterium bifidus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GRRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bifidogenic peptide; protease; treatment; microbe-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 267; DB 20;
100.0%; Pred. No. 2.8e-29;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW93884 standard; peptide; 49 AA
                                                                                                                                                     Claim 2; Page 3; 25pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-EP05899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 48; Conservative
                       Forssmann W, Liepke C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bifidobacterium bifidus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaginal microflora,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
Disulfide-bond
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16-SEP-1997;
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This invention describes milk-derived bifidogenic peptides and their active derivatives or fragments, and combinations of them produced by chemical coupling. Such are produced from bovine or human milk by treatment for 2 hr with proteases, then centrifuging to remove fat and aciditying to pH 2 to precipitate proteins. The solution phase is then subjected to reverse-phase high-performance liquid chromatography (HPLC) and cation-exchange HPLC, the fractions adjusted to salt content below 25 mM (by dialysis or reverse-phase HPLC) and tested for activity by growing Bifidobacterium bifidus and Escherichia coll in presence of the fractions. Those fractions for which (Bw-BD)-(Ew-ED) is at least 0.15 are selected where Bw = germ count after 16 hr culture of E. coll in 3 g/l tryptic broth containing peptide at 0.2 mg/ml, BD = germ count under similar conditions in a peptide-free control, Ew = germ count after 16 hr culture of E. coll in 3 g/l tryptic broth containing peptide at 0.2 mg/ml, ED = germ count under similar conditions in a peptide-free control. The peptides Aww3865-w3888 are used to treat microbe-related diseases caused by bacteria, fungi, yeast, protozoa, viruses, mycoplasma, filaria and plasmodla, e.g. infections, inflammation, microbially induced tumours or degenerative disorders, diarrhoea, colic, abnormalities in oral, intestinal or vaginal microflora, or caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endotoxin neutralisation; Gram negative bacterium; lipopolysaccharide;
LPS; antibacterial; antifungal; sepsis; septic shock; tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lactoferrin fragment; host-defence peptide; antimicrobial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial/endotoxin neutralizing polypeptide generated by
                                                                                                   that stimulate Bifidobacterium bifidus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 97.8%; Score 261; DB 20; Best Local Similarity 100.0%; Pred. No. 1.9e-28; Matches 47; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human lactoferrin fragment, SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB22817 standard; protein; 51
                                                                                                                                       Claim 2; Page 3; 25pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JAN-2000; 2000WO-IB00271
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                                                                                                   peptides
                                                          WPI; 1999-244022/20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 AA;
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                                                                                                 Milk-derived
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                                                                                          The invention relates to proteolytic fragments of lactoferrin (LF) and variants thereof which act as host-defence peptides, having antimicrobial and endotoxin-neutralising activity. The peptides are useful for treatment of bacterial and fungal infections, and may be particularly used for treating sepsis, tuberculosis and leprosy. The peptides are also useful for treating a variety of products at risk of contamination with microorganisms and endotoxin (lipopolysaccharide, LPS), such as food products, tissue, living cells, blood, drugs, glassware and surgical equipment. Sequences AAB22817 and AAB2282-B22827 represent specifically claimed human lactoferrin derived polypeptides of the invention. The present sequence is a 6 kD fragment of human lactoferrin comprising the N-terminal 51 residues produced via cathepsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or may residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or may residue.
proteolytic digestion of lactoferrin, useful for treatment of bacterial and fungal infections, and for preventing contamination of e.g. food products, living cells, and blood -
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "each Cys residue may be in reduced form
form a disulphide bond with another Cys
A 10-46 disulphide bond is exemplified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "each Cys residue may be in reduced form
form a disulphide bond with another Cys
A 20-37 disulphide bond is exemplified"
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                                                                                                                                                                                                                                                                                                                                                                                                                                48
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         2 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA
                                                                                                                                                                                                                                                                                                                                                        97.8%; Score 261; DB 21;
100.0%; Pred. No. 2e-28;
1ve 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR87906 standard; peptide; 52
                                                               Claim 5; Page 8; 90pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93JP-0240284.
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                                                                                                                                                                                                                                                                                                                                                                                           47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human lactoferrin (1-52).
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/note=
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/note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiviral; lactoferrin;
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                                                                                                                                                                                                                                                                                                                                                                             Sest Local Similarity
                                                                                                                                                                                                                                                                                                                             51 AA;
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Disulfide-bond
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The sequence is one of six peptides disclosed as having inhibitory

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effect against viral infection. The peptides are derived from lactoferrin. Their activity is demonstrated against cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide(s) derived from human lactoferrin - are useful as
uno:activators, esp. for preventing infection by cytomegalovirus
                                                                                                                                                                                                                                                                                                             lmmunoactivator; antiviral; cytomegalovirus; cosmetic; food; feed;
lymphocyte blastogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is one of four new peptides (see AAR91191 - AAR91193) obtained by enzymatically decomposing lactoferrin using procease. The peptides are immunoactivators which induce blastogenesis of lymphocytes and are particularly useful for treating cytomegalovirus infection. They can be used in drugs and cosmetics and can be added to foods and feeds.
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                                                                                                                                                                                                                                                                                                                                                                                        10..46 /note= "optionally this bond may be reduced" 20..37 /note= "optionally this bond may be reduced"
                                                                                                                               Length 52;
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                                                                                                                 2 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA
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                                                                 DB 16;
2e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.8%; Score 261; DB 17
100.0%; Pred. No. 2e-28;
Live 0; Mismatches
                                                        97.8%; Scc. 100.0%; Pred. No. c. 100.0%; Pred. No. c. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                    Lactoferrin decomposition peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 2; 11pp; Japanese.
                                                                                                                                                                                                       AAR91192 standard; peptide; 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR88218 standard; peptide; 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94JP-0232026
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                                                                                                                                                                                                                                                          (first entry)
                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immuno:activators, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-205535/21.
                                                                         Local Similarity
les 47; Conserv
                                        52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 AA;
                                                                                                                                                                                                                                                                                                                                                                                        Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP08073499-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-SEP-1994;
                                                                                                                                                                                                                                                          06-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAR-1996
                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                         Sequence
                                                                                                                                                                                                                                  AAR91192;
                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                            Best Loca
Matches
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AAR88218
ID AAR8
                                                                                                                                                                                 RESULT 5
                                                                                                                                                                                              AAR91192
  88.88
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The sequence represents the human lactoferrin (hLF) protein variant hLF-2N. The invention relates to novel methods of treatment using high doses of lactoferrin. The methods of the invention are useful for the treatment or prophylaxis of infectious diseases, inflammatory diseases and excess of heparin e.g. gastroenteritis, inflammatory bowel disease, sepsis, anaemia, myelopoieses, reducing reperfusion injury, cytokine release and proteoglycan-mediated entry of virus into cells. The advantage of the method is that the patient is substantially free of side effect responses to administration of lactoferrin. Therefore large doses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of lactoferrin can be administered. Note: The present sequence is not shown in the specification but is derived from human wild-type lactoferrin sequence given in the sequence
                                                                                                                                                                                                                                                                                                                         treatment of infectious diseases, inflammatory heparin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; feed improvement; plant-derived feed; antibiotic; additive; anti-microbial; poultry; lactoferrin; flour; malt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 261; DB 22;
Pred. No. 3.7e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Encoded'by CTG TAC CTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.8%; Sco...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                           (PHAR-) PHARMING INTELLECTUAL PROPERTY BV
26..29
/label- Cationic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key Location/Qualifiers
Misc-difference 319..320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE27884 standard; Protein; 690 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human codon optimised lactoferrin.
                                                                                                                                                                                                                                                                                                                                                                                             Claim 10; Page -; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          listing of the specification.
                                                                                                                               27-MAR-2001; 2001WO-NL00253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-FEB-2002; 2002WO-US04919
                                                                                                                                                                    2000EP-0201110
                                                                                                                                                                                      2000US-193352P
                                                                                                                                                                                                                                                            Nuijens JH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Best Local Similarity 100.
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                     Use of lactoferrin for diseases and excess of
                                                                                                                                                                                                                                                                                                 WPI; 2001-648424/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             690 AA;
                                                      WO200172322-A2.
                                                                                                                                                                                                                                                            Van Bree JBMM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200263975-A2
                                                                                                                                                                                    27-MAR-2000;
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                                                                                                                                                                    27-MAR-2000;
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 Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A recombinant vector in which a DNA sequence encoding at least the generic lactoferrisin antibacterial peptide AAR88116 (specific examples of which are given in AAR84083-85) is inserted, pref. downstream of the vector's regulatory sequence, is claimed. Pref. examples of amino acid sequences contg. the above peptide are given in AAR88217/18. The regulatory sequence is the tac promoter from shuttle vector pSEZ2, the GALI promoter from vector pKOM2 or Rous Sarcoma Virus long terminal repeat from vector pRSVNot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used to prepare an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; lactoferrin; hLF; infectious disease; inflammatory disease;
                                                                                                                             Recombinant vector; human; lactoferrisin; antibacterial peptide; regulatory sequence; tac; promoter; shuttle; vector; pGEX2; GAL1; pFOWE; Rous Sarcoma Virus; long terminal repeat; pRSVNot; lactoferricin.
                                                                                            Amino acid sequence contg. lactoferrisin antibacterial peptide.
                                                                                                                                                                                                                                                            Location/Qualifiers
19..29
/note= "lactoferrisin antibacterial peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant vector contg. lactoferrisin gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 261; DB 16;
Pred. No. 2.1e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG77908 standard; protein; 690 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human lactoferrin variant hLF-2N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 11; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MORG ) MORINAGA MILK IND CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.88;
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                                                      12-JUN-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibacterial peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 AA;
                                                                                                                                                                                                                           Homo saptens
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                                                                                                                                                                                                                                                                                                                                                                                                             11-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1994;
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                   AAR88218;
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AAG77908 RESULT

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Length 690;

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recovering transgenic grains containing polypeptide from transformed
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Best Local Similarity 100.
Matches 47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-161129/14.
                                                                                                                                                                                                                                                                                                                                                                         690 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ58122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                            Seguence
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                                              Exampe
               plant
g
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                                                                                                                                                                                                                                                          The invention relates to improved feed for production animals, comprising one or more plant-derived feed ingredients, substantially unsupplemented with small-molecule antibiotics and as an additive a seed composition containing a flour, extract or malt obtained from mature monocot seeds and one or more heterologous seed-produced antimicrobial proteins in substantially unpurified form. The invention is useful as a feed for production animals such as poultry and hoofed farm animals. The present sequence is human codon optimised lactoferrin. This sequence is used in the invention.
                                                                                                                                               Improved feed for production animals, comprising plant-derived feed ingredients, and seed composition containing flour, extract, or malt from mature monocot seeds and heterologous seed-produced anti-microbial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transformed plant; heterologous transcription factor; transgenic plant; seed protein; protein expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Producing heterologous polypeptide in plant grain, by culturing transformed plant to form a grain-producing transforming plant, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              97.8%; Score 261; DB 23; Length 690; 100.0%; Pred. No. 3.7e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. ...
                                                                                                                                                                                                                                   Example 7; Page 148-150; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Codon optimised lactoferrin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ą
                                                                                     Hagie FE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG80724 standard; Protein; 690
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14-FEB-2001; 2001US-269199P.
32-MAY-2001; 2001US-0847232.
          14-FEB-2001; 2001US-269188P. 02-MAY-2001; 2001US-0847232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-2002; 2002WO-US04909
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                                                      (VENT-) VENTRIA BIOSCIENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.0
                                                                                    Huang N, Rodriguez RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-657592/70.
N-PSDB; ABS66515.
                                                                                                              WPI; 2002-682708/73.
N-PSDB; AAD45297.
                                                                                                                                                                                                                                                                                                                                                                                                                  690 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huang N, Yang D;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                     proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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The invention describes a method of producing a heterologous polypeptide

(1) in a grain of a plant, comprising culturing a transformed plant (P1) comprising a first chimer; gene, and optionally, at least one heterologous transcription factor that is capable of enhancing the expression of the chimeric gene, to form a grain producing transforming plant (P2), and recovering transgenic grains containing (I) from P2.

The method is useful for producing heterologous polypeptide in a grain of a plant. (I) is a non-plant storage, human or non-human animal, milk or other than a milk polypeptide, antibodies, cytokines, lymphokines, con other than a milk polypeptide, antibodies, cytokines, lymphokines, anti-infectives, or cytotoxins, or anti-inflammatory molecule or intestinal trafoll factor (TFF) or its active fragment. Preferably, (I) is lactoferrin, lysozyme, lactoferricin, ITF, epidermal growth factor (GGF), keratinocyte growth factor (KGF), insulin-like growth factor (GGF), heratinocyte growth factor (KGF), insulin-like growth factor (GGF), beta-lactoglobulin, alpha-casein, haptocorrin, lactoperoxidase, alpha-l-antitrypsin, immunoglobulins, alpha-lactalbumin, fibrinogen or protesse inhibitor. This is the anino acid sequence of a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of human lactoferrin. The invention relates to a synthetic gene (see AAZ58122) that encodes human lactoferrin but which has codon usage designed to maximise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 690;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         associated with method of producing a transgenic plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 261; DB 23;
Pred. No. 3.7e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 73-77; 93pp; English.
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15; Page 117; 230pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY58733 standard; Protein; 692 AA
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Query Match
Best Local S:
Matches 47,
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                                                                                                                  RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the invention are useful for the treatment or prophylaxis of infectious diseases, inflammatory diseases and excess of heparin e.g. gastroenteritis, inflammatory bowel disease, sepsis, anaemia, myelopoleses, reducing reperfusion injury, cytokine release and proteoglycan-mediated entry of virus into cells. The advantage of the method is that the patient is substantially free of side effect responses to administration of lactoferrin. Therefore large doses of lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents the human lactoferrin (h.F.) protein. The methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treatment of infectious diseases, inflammatory
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                            Human; lactoferrin; hLF; infectious disease; inflammatory disease; excess of heparin; gastroenteritis; inflammatory bowel disease; sepsis; anaemia; myelopolesis; reperfusion injury; cytokine release;
          lactoferrin in a tissue-specific manner, especially in the seeds, can be used in processes for the production of functional vegetal milk, fruit juices, fruit and/or vegetable homogenized foods (claimed). The transgenic plants are selected from solanaceae, cereals, leguminosae, fruit bearing plants and horticultural plants, especially soybean, tobacco and rice.
                                                                                                                                       ö
                                                                                                              Length 692;
                                                                                                                                                        2 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA 48
                                                                                                                                                                      Indels
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0
                                                                                                             97.8%; Score 261; DB 21;
100.0%; Pred. No. 3.7e-27;
ive 0; Mismatches 0;
 Transgenic plants that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BV.
                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Cationic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                               28.31
/label= Cationic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PHAR-) PHARMING INTELLECTUAL PROPERTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 26; Page 47-49; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                     AAG77906 standard; protein; 692 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of lactoferrin for treatmer
diseases and excess of heparin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-MAR-2000; 2000EP-0201110.
27-MAR-2000; 2000US-193352P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-2001; 2001WO-NL00253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Van Bree JBMM, Nuijens JH;
                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                         Similarity 100.
  expression in plants.
                                                                                                                                                                                                                                                                                                                         Human; lactoferrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-648424/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  can be administered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       692 AA;
                                                                                        692 AA;
                                                                                                                                                                                                                                                                                                         Human lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200172322-A2.
                                                                                                                                                                                                                                                                                                                                                                proteoglycan.
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                18-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-OCT-2001
                                                                                                                                                                                                                                                           AAG77906;
                                                                                        Sequence
                                                                                                             Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human lactoferrin his protein (represented by the present sequence).

N-terminal his peptides have antimicrobial activity. The peptides of the invention are used to treat microbial infections, especially infections by gram positive or negative bacteria, particularly listeria, staphylococcus, Riebsiella or Escherichia species, especially infections in monocytogenes, a ureus and E. coli. Other uses include reducing inflammatory response by neutralising heparin or Ilpopolysaccharide or by reducing cytokine production and neutrophil degranulation, inhibiting entry of viruses such as cytomegalovirus, herpes simplex virus 1 or HIV into cells, inhibiting myelopolesis and reducing production of GM-CSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptides comprising the N-terminal region of human lactoferrin protein exhibit higher antimicrobial activity than the full length
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1..27
/note= "Fragments of the N-terminal are specifically referred to in the claims"
                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; lactoferrin; hLF; N-terminal; antimicrobial; heparin; inflammatory response; cytokine production reduction; neutrophil degranulation; myelopoiesis inhibition.
     Length 692;
                                                                                                                                      Length 692;
                                                                                                        2 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein exhibit higher antimicrobial activity than the protein and are useful to treat bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 granulocyte/macrophage colony stimulating factor).
                                                         ö
  DB 22;
3.7e-27;
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Pred. No. 3.7e-27;
97.8%; Score 261; DB
100.0%; Pred. No. 3.7
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PHAR-) PHARMING INTELLECTUAL PROPERTY BV.
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/label- Cationic_domain
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/label= Cationic_domain
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                                                                                                                                                                                                                                                                                           AAB97382 standard; protein; 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nibbering PH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.8%; S
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-NOV-2000; 2000WO-NL00821
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99US-0164975
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                           1 Similarity 100.
47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human lactoferrin (hLF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-335909/35.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Van Berkel PHC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200134641-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-NOV-1999;
11-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                 17-AUG-2001
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                                                                                                                                                                                                                                                                                                                                               AAB97382;
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Matches

à g AAE28002;

RESULT 13

AAE28002

infant Human;

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anti-bacterial; anti-viral; anti-fungal; Colony stimulating factor; CSF; release; leukaemia; breast cancer; hormonal regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA encoding human lactoferrin (AAR85146) was isolated from a hums mammary gland library and inserted into vector publis. Expression in Pichia pastoris GTS 115 (Hish allowed the prodm. of large amounts of the lactoferrin protein, useful as an antiseptic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Insertion, c.f. B.F.Anderson et al, 1989"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated DNA encoding human lactoferrin protein - useful for inhibiting microbial growth and iron deficiency, and for sequestering iron or retarding food spoilage.
                                                                                                                                                                                antiseptic; dietary supplement; iron sequestration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.8%; Score 261; DB 16;
100.0%; Pred. No. 3.7e-27;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human lactoferrin deduced from clone HLF 1212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kurecki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 3a-d; 43pp; English.
                          AAR85146 standard; Protein; 693 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR22423 standard; Protein; 705 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kruzel ML,
                                                                                                                                                                                                                                                                                                                                                        95WO-US05653.
                                                                                                                                                                                                                                                                                                                                                                                            94US-0238445.
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(updated)
(first entry)
                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  (FERR-) FERRODYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 100.
47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dietary supplement, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gollnick P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-403881/51:
N-PSDB; AAT02999.
                                                                                                                                            Lactoferrin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     693 AA;
                                                                                                                                                                                                  Pichia pastoris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                            WO9530339-A1.
                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                      05-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                          05-MAY-1994;
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                                                                                                    02-FEB-1996
                                                                                                                                                                                                                                                                                                                16-NOV-1995
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05-AUG-1992
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                                                                AAR85146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Doyle D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR22423;
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Best Local
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AAR22423
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        AAR85146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a nutritionally enhanced food comprising one or more plant-derived food ingredients, and as an additive, a seed composition containing a flour, extract, or malt obtained from mature monocot seeds and one or more seed-produced human milk proteins in additive compositions are useful for improving infant formula. Infant formulas containing the recombinant human milk proteins are useful in supplementing or enhancing the diet of infants, particularly very low birth weight infants. The present sequence is human codon optimised lactoferrin.
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /noce "These amino acid residues are absent in the sequence shown as SEQ ID NO:2 in sequence listing of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                            plant-derived food; flour; malt; monocot seed; milk protein; formula; lactoferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         improving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the diet of infants,
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                                    2 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA 48
                                                          Length 692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA 48
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100.0%; Pred. No. 3.7e-27;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nutritionally enhanced food compositions, infant formula, or supplementing or enhancing particularly very-low birth weight infants
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
320..321
/note= "These amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 9; Page 104; 179pp; English.
                                                                                                                                                                      AAE28002 standard; Protein; 692 AA.
                                                                                                                                                                                                                                                                                      Human codon optimised lactoferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hagie FE;
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                                                                                                                                                                                                                                                (first entry)
Conservative
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N-PSDB; AAD44922.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
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                                                                                                                                                                                                                                                13-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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Sequence Query Match Best\_Local Matches 4

RESULT 14

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Gaps

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Indels

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Length 693;

us-09-508-095-19.rag

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A Clonetech cDNA library from normal human breast tissue (will was plated in host cells 71090, filter-lifted and probed with mouse lactoferrin cDNA 7267. Positive clones were plaque-purified and the lactoferrin cDNA 7267. Positive clones were plaque-purified and the crescambinant clones were transformed into XLI Blue cells. The recombinant clones were transformed into XLI Blue cells. The longest insert (HLF 1212) was sequenced and was 2117bp in length. The amino acid sequence coded for by HLF 1212 has 4 sites that differ from the previously published revised amino acid sequence cells from the protein (B.F.Anderson et al., J.Mol.BHOL. 209: 711-734, 1989). Also contained within HLF 1212, but not in any of the other partially sequenced isolates, is a deleted cytosine at C bp 2097 (AA 699) which caused a frameshift at the 3' end of the coding CC sequence. The deletion is thought to be either a cloning artefact or a rare species of mRNA. See also AAQ23454 and AAQ23455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or a rare species of mRNA. See also AA023454 and AA023455. (Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent
                                                                     218
/note= "Substitution, c.f. B.F.Anderson et al.,1989"
/note= "Substitution, c.f. B.F.Anderson et al, 1989"
Misc-difference 55
                                                  /note= "Substitution, c.f. B.F.Anderson et al.,1989"
                                                                                                                                                                                                                                                                                                                                                                                                                    Human lactoferrin gene and promoter - used for producing protein for treating e.g. AIDS, neutropenia, skin infections, vaginal infections or septic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .com/dwp1/updates/nt1s_us.html.)
                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Fig 10; 55pp; English.
                                                                                                                                                                                                           91US-0707502.
                                                                                                                                                                                                                                                 91US-0707502.
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                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-113934/14.
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                                                                     Misc-difference
                                                                                                                           USN7707502-N
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2 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA 48 g ò

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Gaps

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0; Indels

97.8%; Score 261; DB 13; 100.0%; Pred. No. 3.8e-27; tive 0; Mismatches 0;

Query Match Best Local Similarity 100. Matches 47; Conservative

Query Match

Length 705;

Search completed: August 11, 2003, 08:18:24 Job time : 36.9515 secs

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August 11, 2003, 08:16:37; search time 19:1068 Seconds (without alignments) 106.293 Million cell updates/sec
                                                                                                                                                                                         US-09-508-095-19
267
1 GRRRSVQWCAVSQPEATKCF.....VRGPPVSCIKRDSPIQCIQA 48
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                328717 seqs, 42310858 residues
                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                    Sednence:
                                                                                                                Run on:
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

328717

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PcTuS\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PcTuS\_COMB.pep:\* Issued\_Patents\_AA: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		4000	1144	Appla	Appli	App11	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	App 1	Appl 1	Appli	Appli	Appli	Appli	App11	App11	Appli	Appli	Appli	App 1	App11	Appli
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SUMMAKIES		-08-464-182A	-406-271	112 -08 -134 -586 -3	1471-622	7 C Q _ T 7 % _	-932-190	3-655-640-	-655-640	-154-019	-461-333	-464-167	-158-313	US-08-476-798-	08-464-182A	US-08-406-271-5	US-09-017-043A	08-154-019-	-461-333-	464-167	12	7	-145-681-	US-08-250-308-	3-453-703-2	-456-106	US-08-456-108-	-265-577	361
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ø	Query Match	97.8	97.8	97.8	9.70		97.8	97.8	97.8	97.8	97.8	97.8	97.8	97.8	97.4	97.4	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1
	Score	261	261	261	261	100	107	761	261	261	261	261	261	261	260	260	254	254	254	254	254	254	254	254	254	254	254	254	254
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Sequence 6. Appli	, 4	Segmence 7. Appli	Sequence 8. Appli	Sequence 8 Appli	Sequence 30. Appl	Sequence 29. April	) [		- 2	Sequence 17. Appl	0	10	7.7	Segmence 4. Appli	4	Sequence 4 Apply	Sequence 22, Appl	
US-08-464-182A-6	US-08-406-271-6	US-08-693-274A-7	US-07-755-161A-8	US-07-891-174-8	US-08-256-771-30	US-08-381-984-29	US-08-693-274A-10	US-09-017-043A-5	US-08-464-182A-17	US-08-406-271-17	US-07-755-161A-10	US-07-891-174-10	US-08-204-487-7	US-08-464-182A-4	US-08-406-271-4	US-09-017-043A-4	US-08-464-182A-22	
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47	47	20	36	36	36	36	48	20	25	52	25	25	25	30	30	21	53	
94.4	94.4	93.6	74.9	74.9	74.9	74.9	59.6	9.65	59.6	29.6	53.2	53.2	53.2	52.8	52.8	50.2	50.2	
252	252	250	200	200	200	200	159	159	159	159	142	142	142	141	141	134	134	
28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

ESULT 1:
IS-08-464-182A-2
Sequence 2, Application US/08464182A
Patent No. 5849885
GENERAL INFORMATION:
APPLICANT: Nuijens, Jan H.
APPLICANT: Van Veen, Harry H.
TITLE OF INVENTION: Isolation of Lactoferrin from Milk
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LIP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SORTWARE: Datentin Release #1 0 Vorsion #1 20

Release #1.0, Version #1.30 CIASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,321
FILING DATE: 16-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 06994-004920US
TELECOMMUNICATION INFORMATION: UMBER: US/08/464,182A 05-JUN-1995 FILING DATE: 530
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,271
FILING DATE: 09-MAR-1995 TELEPHONE (650) 326-2400
TELEPAX: (650) 326-2422
TELEPAX: (650) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acids
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE: SOFTWARE: Patentin Re CURRENT APPLICATION DATA APPLICATION NUMBER: U FILING DATE: 05-JUN-1

NAME/KEY: Peptide LOCATION: 1..54 OTHER INFORMATION: /note= "HLF cDNA of GPE"

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STREET: 400 Seventh St. N.W. CITY: Washington D.C. COUNTRY: U.S.A. ZIP: 21004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09421632
Patent No. 6277817
                                                                      APPLICANT: Gollnick, Paul D. APPLICANT: DOYLE, Darrell J. TITLE OF INVENTION: Lactoferri NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: ADDRESSEE: Jacobson, Price,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                          2 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA 48
                                                                                                                                                       3 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA 49
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8e-29;
nes 0; Indels
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100.0%; Pred. No. 8e-29;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       ALDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: One Market Plaza, Steuart Street Tower, 20th CITY: San Francisco STREE: CA Francisco STREET: CA Francisco STREET: CA Francisco STREET: CA Francisco STREET: CA Francisco
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Nuyens, Jan H.
APPLICANT: Van Veen, Harry H.
TITLE OF INVENTION: ISOlation of Lactoferrin from Milk
NUMBER OF SEQUENCE: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and CREW LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,271
FILING DATE: 09-MAR-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: Peptide
; LOCATION: 1..54
; OTHER INFORMATION: /note= "HLF cDNA of GPE"
US-08-406-271-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION: 330
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,321
FILING DATE: 16-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: APPLE, RANDOIN T.
REGISTRATION NUMBER: 36,429
REFERENCE/POCKET NUMBER: 016994-004910
TELECOMMUNICATION INFORMATION:
TELEPRAX: (415) 326-240
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERRISTICS:
LENGTH: 54 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

97.8%; Score 261; DB
Best Local Similarity 100.0%; Pred. No. 8e-
Matches 47; Conservative 0; Mismatches
                                      Query Match 97.8%; Score 261; DF Best Local Similarity 100.0%; Pred. No. 8e-Matches 47; Conservative 0; Mismatches
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                          Sequence 2, Application US/08406271 Patent No. 5919913 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08724586
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Applic
Patent No. 6066469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94105
US-08-464-182A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-08-724-586-2
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Gaps
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APPLICANT: Kruzel, Marian L.
APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
TITLE OF INVENTION: Lactoferrin
Cloning, Expression, and Uses of Human
Lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA 48
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                                                                                                                                                 CONTRET: 400 Seventh St. N.W.

STREET: 400 Seventh St. N.W.

CITY: Washington D.C.

COUNTRY: U.S.A.

ZIP: 2004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724,586

FILING DATE: 30-SEPT-1996

CLASSIFICATION 1435

PRIOR APPLICATION 1994

ATTORNEY/AGENT USS-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 97.8%; Score 261; DB 3; Best Local Similarity 100.0%; Pred. No. 1.4e-27; Matches 47; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/COCKET NUMBER: 10505/P58185C
TELECOMMUICATION INFORMATION:
TELEPHONE: (202) 638-666
TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
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Gaps
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                                                                                                                                                                                                      2 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA 48
                                                                                                                                                                                                                         Length 694;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                   Score 261; DB 4;
Pred. No. 1.4e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: 1100 NEW YORK AVE. N.W., NINTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 261; DB 2;
Pred. No. 1.5e-27;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WTS/5683/98019/SAP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) R61-2000
                                                                                                                    97.8%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Teng, Christina
APPLICANT: Panella, Timothy J.
TITLE OF INVENTION: HUMAN LACTOFERRIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,640
FILLING DATE: 30-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/992,538
FILING DATE: December 17, 1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 26,581
                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08655640 Patent No. 5948613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08655640; Patent No. 5948613; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity 100.0%; P
47; Conservative 0;
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 705 amino acids amino acids
                                                                                                                         Ouery Match
Best Local Similarity 100.0
Matches 47; Conservative
                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) MOLECULE TYPE: protein US-08-655-640-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 47; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1100 NEW CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                           US-09-932-190-2
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Patent No. 6455687
GENERAL INPORMATION:
APPLICANT: Kurecki, Tomasz
Gollinck, Paul D.
Doyle, Darrell J.
TILE OF INVENTION: Cloning, Expression, and Uses of Human
Lactoferrin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: 05/09/932,190
FILING DATE: 17-Aug-2001
CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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CORRESPONDENCE ADDRESS:
STREET: 400 Seventh St. N.W.
COTY: Washington D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Player, William E. REGISTRATION NUMBER: 31,409 REFERENCE/DOCKET NUMBER: 10505/P58185C
                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10505/P58185C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEGUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-5EPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MXY-1994
CURRENT APPLICATION DATA:
                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/724,586
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100.08; Pre-
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LENGTH: 694 amino acids
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Best Local Similarity 100.(
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-421-632-2
                                                                                                                                                                                                                                                                                                                              amino acid
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APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA 68
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One Market Plaza, Steuart Tower, Suite 2000
                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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SOFTWARR: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
97.8%; Score 261; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.5e-27;
Matches 47; Conservative 0; Mismatches 0;
                                                                                                       PAPLICATION NUMBER: US/08/154,019
FILING DATE: 16-NOV-1993
CLASSIPTCATION: 435
FRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/461,333
FILING DATE: 05-UN-1995
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe 0.
REGISTRATION NUMBER: 37,505
REGISTRATION NUMBER: 16994-00312.
TELECOMMUNICATION NUMBER: 16994-00312.
TELECOMMUNICATION NUMBER: 16994-00312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08461333
Patent No. 5741957
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Heyneker, Herbert L.
Platenburg, Gerald
Lee, Sang He
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIble
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 711 amino acids amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-154-019-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
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SOFTWARE: Patentl
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APPLICANT: Deboer
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US-08-461-333-4
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The Market Plaza, Steuart Tower, Suite 2000
San Francisco
California
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: ENDAPY disk
COMPUTER: ENDAPY disk
COMPUTER: ENDAPY disk
COMPUTER: ENDAPY
COMPUTER: DAN FOLDOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/655,640
FILING DATE: 30-MAY-1996
CLASSIFICATION NUMBER: 07/992,538
FILING DATE: December 17, 1992
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WIS/5683/98019/SAP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 97.8%; Score 261; DB 2; 18est Local Similarity 100.0%; Pred. No. 1.5e-27; Matches 47; Conservative 0; Mismatches 0;
                                                                                                                                                          ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVE. N.W., NINTH FLOOR
CITY: WASHINGTON
APPLICANT: Teng, Christina
APPLICANT: Panella, Timothy J.
TITLE OF INVENTION: HOMAN LACTOFERRIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHWAY.
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Patent No. 5633076
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
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IBM PC compatible
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TELEFAX: (202) 822-0944
TELEEX: (714627 CUSH
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein US-08-655-640-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                   AY: USA
20005-3918
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Gaps

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APPLICANT: "-cyneker, Herbert L.
APPLICANT: Datenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pleper, Frank
APPLICANT: Teper, Frank
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
VORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend and Crew
STREET: One Market plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 711;
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UNRENT APPLICATION DATA:
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100.0%; Pred. No. 1.5e-27;
Live 0; Mismatches 0;
      APPLICATION DATE:
FILING DATE:
FILING DATE:
FILING DATE:
APPLICATION NUMBER: US 07/619,131
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
TO NOW-1990
PRIOR APPLICATION NUMBER: US 07/44,745
FILING DATE:
FILING DATE:
TAGNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 16994-0031:
TELECOMMUNICATION:
TELEPHONE: 415-543-9600
TELEPRAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 4:
CFOURENCE CHARACTERISTICS:
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2IP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"MUTTER: IBM PC compatible
""CTFR: COMPUTER: 100 PC compatible
""CTFR: COMPATIBLE PC COMPATIBLE PC COMPATIBLE PC COMPATIBLE PC COMPATIBLE PC POS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09158313
Patent No. 6066725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-NOV-1990
                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 711 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-464-167-4
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US-09-158-313-4
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APPLICANT: Pieper, Frank
APPLICANT: Kinmenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                     PRICE APPLICATION UNBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUBBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATONNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe 0.
REGISTRATION NUMBER: 37,505
REGISTRATION NUMBER: 37,505
REGISTRATION INFORMATION:
TELEPOWNUICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
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FILING DATE: 05-JUN-1995
CLASSIFICATION: 800
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Heyneker, Herbert L.
Platenburg, Gerald
Lee, Sang He
Pieper, Frank
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                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 711 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-461-333-4
                    CLASSIFICATION: 800 PRIOR APPLICATION DATA:
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California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Deboer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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APPLICANT:
APPLICANT:
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US-08-464-167-4
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                                                                                                                                                                                                                                         Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 53,
                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Nuljens, Jan H.
APPLICANT: Van Veen, Harry H.
TITLE OF INVENTION: Isolation of Lactoferrin from Milk
NUMBER OF SECUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,182A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,271
FILING DATE: 09-MAR.1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                         DB 3; 1
1.5e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Peptide
LOCATION: 1..53
OTHER INFORMATION: /note= "HLF cDNA Rado"
                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                         Score 261;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.4%; Score 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRICEAR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,321
FILING DATE: 16-FEB-1994
ATORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T:
REFISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 016994-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                         97.8%; Scur
100.0%; Prf
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08464182A
Patent No. 5849885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION TELEPHONE: (650) 326-2400
      TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS: not relevant not relevant
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TELERAX: (650) 326-2422
INPORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 53 amino acids
                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 47; Conservative
                                          415-543-5043
                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-476-798-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 San Francisco
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US-08-464-182A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: S
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Rrimpenfort, Paul J.A.
APPLICANT: Production of Recombinant Polypeptides
TITLE OF INVENTION: Production of Recombinant Methods
NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Townsend and Townsend and Crew
One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRULA: 125. CONFOUND SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE: Patentin Release #1.0, Version #1.25 APPLICATION DATA: APPLICATION NUMBER: US/08/476,798 FILING DATE: 07.-UN-1995 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                Query Match 97.8%; Score 261; DB 3; 1
Best Local Similarity 100.0%; Pred. No. 1.5e-27;
Matches 47; Conservative 0; Mismatches 0;
                                                              NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE, POCKET NUMBER: 1694-003125
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRA: 415-543-5603
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHRACKTERISTICS:
LENGTH: 711 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 01-DEC-1989
ATJORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe 0.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-UNN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-UN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION DATA:
PRIOR DATE: 27-NOV-1550
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
APPLICATION NO 10-DEC-1989
JMBER: US 07/444,745
01-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08476798 Patent No. 6140552 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deboer, Herman A.
APPLICATION NUMBER: US (FILING DATE: 01-DEC-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: One Mainer
CITY: San Francisco
                                                                                                                                                                                                                                                                                                 / MOLECULE TYPE: protein US-09-158-313-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94105
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Search completed: August 11, 2003, 08:19:45 Job time : 20.1068 secs
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                          ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                 CORRESPONDENCE ADDRESS:
                         TITLE OF INVENTION: & NUMBER OF SEQUENCES:
                                                                                                                                           California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                               FILING DATE: 02 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
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                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                             STATE:
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                           Gaps
                       ó,
                                                                                1 GRRRSVQWCAVSNPEATKCFQWQRNMRKVRGPPVSCLKRDSPIQCIQA 48
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; Patent No. 5919913
; GENERAL INFORMATION:
APPLICANT: Nuyens, Jan H.
TITLE OF INVENTION: 1201ation of Lactoferrin from Milk
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: One Market Plaza, Steuart Street Tower, 20th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 260; DB 2; Length 53;
Pred. No. 1.1e-28;
1; Mismatches 1; Indels
                                                             1 GRRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GRRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk Compatible Computible Computible Compatible Corputible System: PC-DOS/MS-DOS SOFTWARE: PAtentin Release #1.0, Version #1.30 CURRENT APPLICATION DAR?:
APPLICATION NUMBER: US/08/406,271 FILING DATE: 09-MAR-1995 CLASSIFICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/198,321 FILING DATE: 16-FEB-1994 FILING DATE: 16-FEB-1994 ATORNEY/AGENT INFORMATION: NAME: Apple, Randolph T. REFERENCE/DOCKET NUMBER: 36,429 REFERENCE/DOCKET NUMBER: 016994-004910 TELECOMMUNICATION INFORMATION:
    Pred. No. 1.1e-28;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: Peptide
; LCCATION: 1..53
; OTHER INFORMATION: /note= "HLF cDNA Rado"
US-08-406-271-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09017043A Patent No. 6333311 GENERAL INFORMATION: APPLICANT: Nuljens, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Nuljens, Jan
APPLICANT: van Berkel, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: not relevant
TOPOLGGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.4%;
95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
Best Local Similarity 95.8%;
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 95.8'
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 53 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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US-09-017-043A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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Gaps
Useful Properties of Human Lactoferrin and Variants Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA
                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,043A FILING DATE: US-FEB-1998 CLASSIFICATION: 514
                                                                                           ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 95.1%; Score 254; DB 4; Best Local Similarity 95.7%; Pred. No. 6.9e-28; Matches 45; Conservative 1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          016994-011010US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,859
FILING DATE: 03-FEB-1997
ATTORNEY AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 016994-0110
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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using sw model OM protein - protein search,

August 11, 2003, 08:17:06 ; Search time 132.35 Seconds Run on:

(without alignments)
46.167 Million cell updates/sec

US-09-508-095-19 267

1 GRRRSVQWCAVSQPEATKCF..... VRGPPVSCIKRDSPIQCIQA 48 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

479057 seqs, 127295195 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

'Ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
'Ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\* ptodata/1/pubpaa/US10C\_PUBCOMB.pep 6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep: 6/ptodata/1/pubpaa/PCTUS\_BUBCOMB.pep: 6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep: 6/ptodata/1/pubpaa/US08\_PUBCOMB.pep: /pubpaa/US09A\_PUBCOMB.pep L/pubpaa/US09B\_PUBCOMB.pep /pubpaa/US09\_NEW\_PUB.pep Published\_Applications\_AA:\* cgn2\_

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Sequence 4. Appli	Sequence 4. Appli	`	200		• •	٠.		Sequence 0, Applit	ט נ ט נ	77	Sequence 23, Appl	Sequence 2. Appli	-	ì	·	sednence 3, Appli
SUMMAKIES			QI	US-10-076-816-4	US-10-077-381-4	US-10-023-096-2	US-09-798-869-20	US-09-738-973-203	US-09-854-133-203	US-10-144-649A-203	13-09-935-642-6	13-09-866-050	TIS-00-708-860-22	77 600 067 60 00	US-09-798-869-23	US-09-798-869-2	US-10-145-651-1	US-09-798-869-6	r c13-cc1-01-011	C-7#9-CCT-OT-CO
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	er (	Query	Match	97.8	97.8	97.8	53.2	44.4	44.4	44.4	44.4	39.9	36.0		13.	32.6	32.2	29.6	7 90	
			Score	261	261	261	142	118.5	118.5	118.5	118.5	106.5	96		2	87	86	79	76.5	
		TEST	NO.	7	~	m	7	S	φ <sup>'</sup>	ŗ	<b>6</b> 0	თ	10		7 1	12	13	14		2

5, 10, 205, 205, 205, 205, 205, 205, 205, 20	Sequence 10, Appl Sequence 3, Appl Sequence 4, Appli	Sequence 4342, A Sequence 17, Appl Sequence 16, Appl Sequence 15, Appl	3, A 4, A 2, A	Sequence 1331, Ap Sequence 248, App Sequence 248, Appl Sequence 87, Appl	7, AF 291, 8, Ap 6308,	Sequence 388, App Sequence 21, Appl Sequence 8748, Ap Sequence 690, App Sequence 88, Appl Sequence 252, Appl	525
11 US-09-847-208-102 9 US-09-891-126-5 9 US-09-509-652-4 9 US-09-030-619-205 0 US-09-017-340-16	1 US-09-798-869-21 1 US-09-798-869-3 1 US-09-798-869-4	US-09-941-314-17 US-09-941-314-16 US-09-941-314-16	10 US-09-941-314-3 10 US-09-941-314-4 10 US-09-941-314-3 9 US-09-925-301-133		US-09-975-719-2 US-09-775-719-2 US-09-798-869-8 US-09-864-761-36	10-080-1/0-3 -10-311-111-2 -10-156-761-8 -09-764-868-6 09-917-340-88	LS US-10-097-065-525
328 328 25 25 25	n n n n a			397 397 14 15	103	132 306 393 173 173	173 ]
282 26.24 26.32 26.33 26.33	222.3	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	6.66 6.66 6.66 6.66	0.0000	5.000	18.7 18.7 18.7 18.7 18.5	18.2
76 70 65 65 65	100 U L	. W W W .	ນ ເນ ເນ ເນ ເນ ເນ	52 53 35 52 55 33 52 55 33	522	50 50 50 50 49.5	48.5
16 11 119 20	22 23 23 24	25 27 27	30 30 31 31 31		333	7 4 4 4 4 4 7 0 4 0 8 4	45

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                                                                                         APPLICANT: Rodrguez, Raymond APPLICANT: Hagie, Frank E. TITLE OF INVENTION: Feed Additive Compositions and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 261; DB 15;
; Pred. No. 5.9e-26;
0; Mismatches 0;
                                                                                                                                                            FILE REFERENCE: 50665-8021.0500
CURRENT APPLICATION NUMBER: US/10/706,816
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/269,188
PRIOR FILING DATE: 2001-02-14
PRIOR PILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-06
PRIOR FILING DATE: 2001-05-06
PRIOR FILING DATE: 2001-05-06
PRIOR FILING DATE: 2000-05-06
NUMBER: OF SEQ ID NOS: 60
SECTRARE: FastSEQ for Windows Version 4.0
; Sequence 4, Application US/10076816; Publication No. US20030056244A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.8%;
100.0%;
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Best Local Similarity 100.
Matches 47; Conservative
                                                                     APPLICANT: Huang, Ning
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3 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA 49

RESULT 2

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Gaps

2 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA

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Gaps
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                                                                                                                                                                                                                               Length 694;
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                                                                                                                                                                                                                                                                                                                                        5 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA
                                                                                                                                                                                                                                                                        Indels
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100.0%; Pred. No. 7.3e-12;
ive 0; Mismatches 0;
                                                                                                                                                                                                                             97.8%; Score 261; DB 14;
100.0%; Pred. No. 5.9e-26;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020110563A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVENIBJ(RNSSON
APPLICANT: LARS VORLAND
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Henderson, Robert A
Lodes, Michael J.
Fling, Steven P.
             TELEPHONE: (202) 638-6666
INFORMATION FOR SEQ ID NO: 2: SEGÜENCE CHARACTERIZICS:
LENGTH: 694 amino acids
TYPE: amino acids
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Indirias, Carol Y
Benson, Darin R.
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Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mohamath, Raodoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 25; Conservative
                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 47; Conservative
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                                                                                                                                                             ; MOLECULE TYPE: protein US-10-023-096-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elliot, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                            TOPOLOGY:
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LENGTH: 25
                                                                                                                                                                                                                               Query Match
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APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
TITLE OF INVENTION: Lactoferrin
MUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4. Application US/1007381
Sequence 4. Application US/1007381
GENERAL INFORMATION:
APPLICANT: Huang, Ning
APPLICANT: Hade, Frank E.
TITLE OF INVENTION: Expression of Human Milk Proteins in TITLE OF INVENTION: Expression of Human Milk Proteins in TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 50665-8022 US00
CURRENT APPLICATION NUMBER: US/10/07/381
CURRENT APPLICATION NUMBER: US 60/269,199
PRIOR FILING DATE: 2001-05-14
PRIOR PELING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/266,929
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-03
PRIOR FILING DATE: 2001-05-05
PRIOR FILING DATE: 2001-05-05
SPRIOR FILING DATE: 2001-05-05
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 15;
5.9e-26;
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Washington D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-WAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.8%; SCS_
100.0%; Pre
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31,409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Player, William E REGISTRATION NUMBER: 31
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Best Local Similarity 100.
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CORGANISM: Homo sapiens
US-10-077-381-4
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STREET: 4(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 690
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APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c4U
CURRENT APPLICATION NUMBER: US/09/866,050A
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ IO NOS: 725
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 RSVQWCAVSQPEATKCFQWQRNMRKV---RGPPVSCIKRDSPIQCIQA
                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09935642

FUDLICATION NO. US20030044795A1

GENERAL INFORMATION:
APPLICANT: BYAZLSEN, INGER
APPLICANT: LARSEN, Peter
APPLICANT: STEPHEN, John
TITLE OF INVENTION: Biochemical Markers for the Human
TITLE OF INVENTION: Endometrium
TITLE OF INVENTION: Biochemical Markers for the Human
TITLE OF INVENTION: Endometrium
FILLE REFERENCE: 8969-014
CURRENT FILLING DATE: 1997-09-05
FRIOR APPLICATION NUMBER: PCT/GB97/07324
FRIOR APPLICATION NUMBER: PCT/GB97/0732.8
FRIOR APPLICATION NUMBER: PCT/GB9707132.8
FRIOR PILLING DATE: 1997-04-08
FRIOR FILLING DATE: 1996-09-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
                                                          44.4%; Score 118.5; DB 15;
45.8%; Pred. No. 6.2e-08;
tive 13; Mismatches 10;
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45.8%; Pred. No. 2.8e-07,
tive 13; Mismatches 1(
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                                                     Query Match
Best Local Similarity 45.83
Matches 22; Conservative
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APPLICANT: Watson, James D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-642-6
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Best Local Similarity
Matches 22; Conserva
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Best Local Similarity
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ORGANISM: Mouse
          US-10-144-649A-203
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US-09-866-050A-693
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                                                                                                                                                                                                                                                                                                                                                                                          4 RSVOWCAVSOPEATKCFOWQRNMRKV---RGPPVSCIKRDSPIQCIQA 48
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APPLICANT: Lodes, Michael J.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.475c10
CURRENT APPLICATION NUMBER: US/09/854,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INCORNATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Wang, Tongrong
APPLICANT: Wang, Tongrong
APPLICANT: Fan, Liqun
APPLICANT: Algae, Paul A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .2e-08;
es 10; Indels
                                                                                                                                                                                                                                                                      ; Score 118.5; DB 1
; Pred. No. 6.2e-08;
13; Mismatches 10
FILE REFERENCE: 210121.475C9
CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: FastSEQ for Windows Version 3.0
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SOFTWARE: FastSEQ for Windows Version 3.0
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 203, Application US/09854133
Publication No. US20020183499A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 45.8%;
Matches 22; Conservative 13
                                                                                                                                                                                               ; ORGANISM: Homo sapien US-09-738-973-203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Homo sapien
US-09-854-133-203
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ORGANISM: Homo sapien
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US-10-144-649A-203
                                                                                                                    SEQ ID NO 203
LENGTH: 164
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LENGTH: 164
                                                                                                                                                                      TYPE: PRT
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Gaps

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Indels

Mismatches

13;

20; Conservative

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mann, David
TITLE OF INVENTION: ANTIMICROBIAL/ENDOTOXIN NEUTRALIZING
TITLE OF INVENTION: POLYPETIDE
FITLE OF INVENTION: POLYPETIDE
FILE REFERENCE: 00138.0051.NPUSO0
CURRENT APPLICATION NUMBER: US/10/145,651
PRIOR APPLICATION NUMBER: US/09/245,527
PRIOR FILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    core 87; DB 11; I
Pred. No. 6.9e-05;
                                                                                                                                   APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ(RNSSON
APPLICANT: LARS VORLAND
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRSEEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.6%; Score 87; 100.0%; Pred. No.
                                                           Sequence 2, Application US/09798869 Publication No. US20030022821A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10145651
Publication No. US20030105006A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09798869
Publication No. US20030022821A1
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Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
                                                                                                                    APPLICANT: JOHN SIGURD SVENDSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 PVSCIKRDSPIQCIQA 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 TKCFQWQRNMRKVRG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT;
; ORGANISM: HOMO SAPIENS
US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 15; Conserv
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US-10-145-651-1
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4 RSVQWCAVSQPEATKCFQWQRNMRKV---RGPPVSCIKRDSPIQCIQA 48
                     Length 25;
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52.0%; Pred. No. 4.8e-05;
"":matches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 96; DB 11;
Pred. No. 7.8e-06;
                                                                                                                                 Sequence 22, Application US/09798869
FUDIcation No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: OF SIGNED SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: EALDUR SVEINBLAN
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REPERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
FRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSELSEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQUENCE 23, Application US/09798869.
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: US20030022821A1
APPLICANT: (YSTEIN REKNAL
APPLICANT: (YSTEIN REKNAL
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-05A-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-11
PRIOR FILING DATE: 1999-08-18
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SSOFTWARE: FASTSEQ for Windows Version 4.0
SEO TWANT SECOND
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Best Local Similarity 62.5%;
Matches 15; Conservative
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Best Local Similarity 52.0
Matches 13; Conservative
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US-09-798-869-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: CAPRINE
US-09-798-869-23
                                                                                                                        -869-22
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US-09-798-869-23
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Job time : 132.35 secs
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APPLICANT: Jefferles, Wilfred A.
APPLICANT: McGeer, Patrick I.
APPLICANT: McGeer, Patrick I.
APPLICANT: Rothenberger, Sylvia
APPLICANT: Rothenberger, Sylvia
APPLICANT: Food, Michael R.
APPLICANT: Yamada, Tatauo
APPLICANT: Yamada, Malcolm
TITLE OF INVENTION: Use of p97 and Iron Binding Froteins as Diagnostic and Therapeuti
TITLE REPERCENCE: 7665-48
CURRENT APPLICATION NUMBER: US 09/285,040
PRIOR PRILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: US 08/520,933
PRIOR FILING DATE: 1995-08-31
PRIOR FILING DATE: 1993-07-09
PRIOR FILING DATE: 1993-07-09
PRIOR FILING DATE: 1993-07-09
PRIOR FILING DATE: 1993-07-09
PRIOR APPLICATION NUMBER: US 08/367,224
PRIOR APPLICATION NUMBER: US 08/367,224
PRIOR APPLICATION NUMBER: US 08/367,224
PRIOR APPLICATION NUMBER: US 07/912,291
PRIOR PRIOR PRIOR DATE: 1992-07-10
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                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
OTHER INFORMATION: sequence)
US-09-798-869-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 79; DB 11; Length 15;
Pred. No. 0.00078;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 76.5; DB 15;
Pred. No. 0.091;
8; Mismatches 20;
                APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR PLING DATE: 1998-08-38
PRIOR PLING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: F854SEQ for Windows Version 4.0
BALDUR SVEINBJ(RNSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.7%;
32.6%;
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Best Local Similarity 93.3%;
Matches 14; Conservative
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SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TKCFQWQWNMRKVRG 15
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Best Local Similarity 32.6
Matches 14; Conservative
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US-10-133-642-3
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LENGTH: 15
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Search completed: August 11, 2003, 08:25:41

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

August 11, 2003, 08:16:37 ; Search time 13.0485 Seconds (without alignments) 353.763 Million cell updates/sec

score: Perfect

US-09-508-095-19 267 1 GRRRSVQWGAVSQPEATKCF.....VRGPPVSCIKRDSPIQCIQA 48 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_76:\* Database :

pirl:\* pir2:\* pir3:\* pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	TFRUI.	JC2323	A28438	TFBOL	147228	S01384	TFHUP	A45543	S52107	TFRBP	S49163	S33761	151350	T11749	TFHUM	TFCHE	S12100	A28446	G82630	S29934	AI0832	T19139	C75554	XYRTEA	T24321	T24322	A34589	VCBEM7	T42938
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	Length	711	708	707	708	704	969	698	703	33	694	695	206	64	069	738	705	717	311	551	373	373	546	262	2505	417	419	422	1371	1371
đ	Query Match		60.7			49.6	•	4.	44.2	43.1	41.4	39.1	38.6	28.7	28.7	28.7	28.2	27.0	25.5	22.5	21.3	21.3	21.3	21.0	20.6	20.5	20.3	20.3	20.0	20.0
	Score	261	162	159	134	132.5	120	118.5	118	115	110.5	104.5	103	76.5	76.5	76.5	92	72	68	09	57	57	57	. 95	52	54	54	54	53.5	ω.
	Result No.	-		m	4	2	9	7	œ ·	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

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# ALIGNMENTS

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C;Species: Homo.sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text_change 08-Dec-2000
C;Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000;
                                                                                                                                                                                                                submitted to the EMBL Data Library, March 1994
A) Reference number: G06820
A) Accession: G01394
A) Status: preliminary; translated from GB/EMBL/DDBJ
lactotransferrin precursor [validated] - human
                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-711 <CHO>
                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
                                     N; Alternate names:
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A)Cross-references: EMBL:U07643; NID:9467236; PIDN:AAB60324.1; PID:9467237 R:Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R. Nucleic Acids Res. 18, 5288, 1990
A)Title: Complete nucleotide sequence of human mammary gland lactoferrin. A)Reference number: S11228; MUID:90384839; PMID:2402455

A; Molecule type: mRNA A; Residues: 1.148, T'.150-422, C', 424-711 <REY> A; Cross references: EMBL:X53961; NID:334415; PIDN:CAA37914.1; PID:g34416 B; Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T. Mol. Endocrinol. 6, 1969-1981, 1992 A; Title: Differential molecular mechanism of the estrogen action that regulates lacto A; Reference number: A45401; MUID:93125571; PMID:1480183

A;Molecule type: DNA
A;Residues: 1-15 <TEN>
A;Residues: 1-15 <TEN>
A;Cross-references: GB:S52659; NID:g263311; PIDN:AAB24877.1; PID:g263312
A;Experimental source: placenta
A;Experimental source: placenta
A;Note: sequence extracted from NCBI backbone (NCBIP:122202)
R;Powell, M.J.; Ogden, J.E.

Nucleic Acids Res

A;Title: Nucleotide sequence of human lactoferrin cDNA. A;Reference number: \$10324; MUID:90326549; PMID:2374734

A; Molecule type: mRNA A; Residues: 3-711 <POW>

A;Cross-references: EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412
R;Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.
Biochem. J. 276, 349-355; 1991
A;Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
A;Reference number: S15853; MUID:91264786; PMID:2049066
A;Recession: S15853

A,Status: nucleic acid sequence not shown; not compared with conceptual translation A; Molecule type: mRNA

A; Molecule type: protein A; Residues: 20-28, 'X', 30-31 <ST2>

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Gaps

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48 67

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C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A28438; A41205
R;Pentecost, B.T.; Teng, C.T.
J. Biol. Chem. 262, 10134.10139, 1987
J. Hille: Lactortransferrin is the major estrogen inducible protein of mouse uterine se A;Reference number: A92596; MUID:87280033; PMID:3611056
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C;Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text_change 11-May-2000
C;Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text_change 11-May-2000
C;Accession: 145919; S14674; S14110; S18517; JT0595; S13097; S18518; S13881; PL0148;
R;Tsangy, T.C.: Burns, D.K.; Wang, F.; Pan, Y.
R;Tsang, T.C.: 233, 1991
A;Title: Cloning of a 80-kD advanced glycosylation end product (AGE) binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-144,'V',146-163,'PP',166-339,'A',341-438,'Y',440-513,'R',515-708 <PI1>A;Cross-references: EMBL:X57084; NID:9505; PIDN:CAA40366.1; PID:9506
R;Pierce, A.; Colavizza, D.; Benaissa, M.; Maes, P.; Tartar, A.; Montreull, J.; Splk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A)Cross-references: EMBL:J03298
R)Liu, Y.; Teng, C.T.
J. BAOl. Chem. 266, 21880-21885, 1991
A):Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
A):Reference number: A41205, WUID:92042099; PMID:1939212
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C;Superfamily: transferrin, transferrin repeat homology
C;Superfamily: transferrin; Transferrin repeat homology
C;Reywords: duplication: glycoprotein
F:1-19/Domain: signal sequence #status predicted <SIG>F:20-707/Product: lactotransferrin #status predicted <MAT>F:358-695/Domain: transferrin repeat homology <TRRIZ>F:358-695/Domain: transferrin repeat homology <TRRIZ>F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                            Length 708;
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                                                                                                                                                                                                                                                                               22 RKNVRWCAISLPEWSKCYQWQRRMRKLGAPSITCVRTSALECIRA
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                     Score 162; DB 2; Le
Pred. No. 1.2e-12;
...-rhes 8;
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                                                                                                                                              14; Mismatches
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A; Status: translated from GB/EMBL/DDBJ
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N;Alternate names: lactotransferrin
                                                                60.7%;
52.2%;
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24; Conservative
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A, Molecule type: mRNA
A, Residues: 3-707 <PEN>
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A; Residues: 1-15 <LIU>
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R;Rado, T.A.; Wel, X.; Benz Jr., E.J.
Blood (70, 899.93), 1997
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of many cossion: 807160, MUD:88001031; PMID:3477300
A;Rocession: 807160, MUD:88001031; PMID:3477300
A;Rocession: 807160, MUD:87711 <RAD>
A;Rossion: 807160, MUD:87711 <RAD
A;Rossion: 807160, MUD:87711 <RAD
A;Rossion: 807160, MUD:87711 <RAD
A;Rossion: 807160, MUD:877160, MUD:87661, PMID:87160
A;Rossion: 807160, MUD:87661, PMID:87661, PMID:87160
A;Rossion: 807160, MUD:876661, PMID:87661, PMID:87160
A;Rossion: 807160, MUD:876661, PMID:87661, PMID:87160
A;Rossion: 807160
A;Rossion: 8
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Stywords: duplication; glycoprofeein
359-696/Domain: transferrin repeat homology <TRH2>
252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C; Date: 20 Feb-1995 #sequence_revision 20 Feb-1995 #text_change 07-May-1999
C; Accession: JC2323
R; E Provost, F: Nocart, M.; Guerin, G.; Martin, P.
Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
A; Title: Characterization of the goat lactoferrin cDNA: assignment of the re
A; Reference number: JC2323
A; Molocule type: MRNA
A; Residues: 1-708 <LEP>
C; Superfamily: transferrin; transferrin repeat homology
C; Reywords: duplication; flycoprotein
C; Stywords: duplicatio
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Pred. No. 3.4e-25;
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100.0%; Pred. No. ...
0; Mismatches
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Matches 47; Conserv
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Gaps

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A; Molecule type: protein
A; Residues: 1-8, 'X', 10-11, 'X', 13-15 <BA2>
A; Experimental source: gastric mucosa
A; Experimental source: gastric mucosa
A; Note: the authors suggest transferrin from gastric mucosa may act in dietary iron u
B; Chung, M.C.M.; Chan, S.L.; Shimizu, S.
Int. J. Biochem. 23, 609-616, 1991
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R;Roush, B.D.; Fierke, C.A.
Biochemistry 31, 12536-12542, 1992
A;Title: Purification and characterization of a carbonic anhydrase II inhibitor from A;Reference number: 147228; MUID:93099129; PMID:1463741
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A;Note: 308-Arg was also found
R;Baldwin, G.S.; Bactc, T.; Chandler, R.; Grego, B.; Pedersen, J.; Simpson, R.J
Comp. Biochem. Physiol. B 95, 261-268, 1990
A;Title: Isolation of transferrin from porcine gastric mucosa: comparison with A;Reference number: A60520; MUID:90227903; PMID:2328566
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                         carbonic anhydrase II inhibitor (transferrin homolog) precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Aug-1999
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 11-May-2000
C;Accession: $0.134; A60520; A61573
R;Baldwin, G.S.; Weinstock
Nucleic Acids Res. 16, 8720, 1988
A;Title: Nucleotide sequence of porcine liver transferrin.
A;Reference number: $01384; MUID:88335629; PMID:3419934
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                                                                  Length 708;
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A;Residues: 1-8,'X',10-18,'XE' <CHU>
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein; iron transport; plasma
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                                                              , DB 1;
4.1e-09;
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F;20-350/Domain: transferrin repeat homology <TRH1>
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                                                                                                                             14; Mismatches
                                                              Score 134;
Pred. No. 4
                                                           50.2%;
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                                                                                                                          20; Conservative
                                                                                            Similarity
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A; Residues: 1-704 <ROU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA A; Residues: 1-696 <BAL>
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                                                       Query Match
Best Local
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A; Residues: 20-35; 82-114; 148-163, 'PP', 166-178,'V','P'; 183-190; 205-212; 230-239; 304-339; 59
                                                                                                                                                                                                                                                                                                                                                                                            R; Goodman, R.E.; Schanbacher, F.L. 180, 75-84, 1991 Blochem. Biophys. Res. Commun. 180, 75-84, 1991 A.Fttle: Bovine lactoferrin mRNA: sequence, analysis, and expression in the mammary glant A; Reference number: JT0595; MUID: 92028986; PMID:1718281
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A; Mesidues: 36-60 <BEL>
A; Residues: 36-60 <BEL>
B; Shimazaki, K.; Tanaka, T.; Kon, H.; Oota, K.; Kawaguchi, A.; Maki, Y.; Sato, T.
J. Dairy Sci. 76, 946-955, 1993
A; Title: Separation and characterization of the C-terminal half molecule of bovine lactd
A; Reference number: A56659; MUID:9323156; PMID:8486845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rejman, J.J.; Hegarty, H.M.; Hurley, W.L.
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Title: Purification and characterization of bovine lactoferrin from secretions of the
Reference number: PLO148; WUID:90031466; PMID:2805645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: protein
Residues: 20-47;59-66;132-139;256-277;278,305-332;343-351;361-363;586,587-589;598-619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-65, PG', 68-296, 'S', 298-339, 'A', 341-708 <GOO>
A; Residues: 1-65, PG', 68-296, 'S', 298-339, 'A', 341-708 <GOO>
A; Cross-references: GB-M63502
A; More: the authors translated the codon CCG for residue 66 as Arg and TCT for residue B; Mead, P.E.; Tweedie, J.W.
Nucleic Acids Res. 18, 7167, 1990
A; Title: CDNA and protein sequence of bovine lactoferrin.
A; Reference number: S13097; MUID:91088328; PMID:2263492
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F;28-64,134-217,176-192,179-200,189-202,250-264,367-399,377-390,424-703,444-666,476-551,
F;28-55,Disulfide bonds: #status predicted
F;39,111,211,272/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
F;140/Binding site: carbonate (Arg) #status experimental
F;252,300,387,495,564/Binding site: carbohydrate (Asp) (covalent) #status predicted
F;414,452,545,614/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
F;482/Binding site: carbonate (Arg) #status experimental
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Residues: 20-25;302-308;359-366, X',368-376, X',378 <SHI>
Residues: 20-25;302-308;359-366, X',368-376, X',378 <SHI>
Superfamily: transferrin: transferrin: repeat homology
Keywords: duplication; glycoprotein; iron, iron binding; metalloprotein; milk
1-19/Domain: signal sequence #status predicted <SIG>
1-19/Pomain: algoriansferrin #status experimental <MAT>
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A:Title: Molecular cloning and sequence analysis of bovine lactotransferrin. A:Reference number: S14110; MUID:91160550; PMID:2001696
A:Rocession: S14110
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                                                                                                                                                                                                               A; Residues: 3-144, 'V', 146-339, 'A', 341-438, 'Y', 440-513, 'R', 515-708
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Dimitted to the EMBL Data Library, October 1990
Accession: S13881
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Residues: 28-33,'DS',36-38,'P',40-708 <MEA>
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Residues: 28-38,'P',40-86,'C',88-708 <ME3>
Cross-references: EMBL:X54801
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A;Accession: S18517
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Accession: S18518
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C;Species: Sus scrota domestica (domestic pig)
C;Species: Sus scrota domestica (domestic pig)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 04-Mar-2000
C;Accession: A4554; S24173
R;Alexander, L.J.; Levine, W.B.; Teng, C.T.; Beattie, C.W.
Anim. Genet. 23, 251-256, 1992
A;Reference number: A45543; MUID:92367939; PMID:1503259
A;Reference number: A45543; MUID:92367939; PMID:1503259
A;Accession: A45543; MUID:92367939; PMID:1503259
A;Accession: A45543; MUID:92367939; PMID:1503259
A;Residues: 1-703 A&LE>
A;Experimental source: manmary gland
A;Residues: 1-703 A&LE>
A;Experimental source: manmary gland
A;Note: sequence extracted from NCBI backbone (NCBIN:111151, NCBIP:111153)
R;Lydon, J.P.; O'Malley, B.R.; Saucedo, O.; Lee, T.; Headon, D.R.; Conneely, O.M.
Biochim: Biophys. Acta 1132, 97-99, 1992
A;Title: Nucleotide and primary amino acid sequence of porcine lactoferrin.
A;Reference number: S24173; MUID:92379101; PMID:1511016
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C; Reywords: duplication; glycoprotein; iron transport; metal binding; plasma
C; Reywords: duplication; glycoprotein; iron transport; metal binding; plasma
E; 1-19/Domain: signal sequence *status experimental <ARA>
F; 20-688/Product: transferrin *status experimental <ARA>
F; 20-568/Product: transferrin repeat homology <ARH1>
F; 25-686/Domain: transferrin repeat homology <ARH2>
F; 35-686/Domain: transferrin repeat homology <ARH2>
F; 38-67, 38-58, 137-213, 156-350, 177-193, 180-196, 190-198, 246-260, 358-615, 364-396, 374-387
F; 432, 630/Binding site: carbohydrate (Asn) (covalent) *status experimental
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A;Introns: 15/1; 72/3; 119/1; 168/1; 212/2; 231/1; 290/3; 350/1; 401/3; 433/1; 444/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Molecule type: mRNA
A)Rosidues: 636-696 <RE2>
A)Cross-references: 638-69641; NID:9339988; PIDN:AAA61233.1; PID:9339989
R)Schaeffer, E.; Lucero, M.A.; Jeltsch, J.M.; Py, M.C.; Levin, M.J.; Chambon, P.; Cob
Gene 56, 109-116, 1987
A)Title: Complete structure of the human transferrin gene. Comparison with analogous
A)Reference number: 154011; MUID:88056305; PMID:3678832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 564-698 <RE4>
A;Cross-references: GB:M17614; NID:g339483; PIDN:AAA61148.1; PID:g339486
C;Comment: Each of the two repetitive domains binds a ferric ion and a bicarbonate
                                                        A; Residues: 1-698 <RES>
A; Cross-references: GB:S95936; NID:9248647; PIDN:AAB22049.1; PID:9248648
R; Duguid, J.R.; Bohmont, C.W.; Liu, N.G.; Tourtellotte, W.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 7260-7264, 1989
A; Title: Changes in brain gene expression shared by scrapie and Alzheimer disease.
A; Reference number: 148174; MUID:89386721; PMID:2780570
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A;Molecule type: DNA
A;Residues: 1-72 <RE3.
A;Cross-references: GB:M17611; NID:g339480; PIDN:AAA61147.1; PID:g339485
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               Molecule type: mRNA
Residues: 1-698 <RES>
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A;Gene: GDB:TF
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R;Uzan, G; Frain, M.; Park, I.; Besmond, C.; Maessen, G.; Trepat, J.S.; Zakin, M.M.; Ka Bacchem. Biophys. Res. Commun. 119, 273-281, 1984
A;Title: Molecular cloning and sequence analysis of cDNA for human transferrin.
A;Reference number: A32739; MUID:84153910; PMID:6322780
A;Accession: A32739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferrin precursor [validated] - human

Nalternate names: siderophilin

(Nalternate names: siderophilin

(Nalternate names: siderophilin

(Nalternate names: siderophilin

(Species: Home sapiens (man)

(Species: Home sapiens (man)

(Species: Home sapiens (man)

(Species: Home sapiens (man)

(Nalte: 15-Oct-1982 #sequence_revision 30-Sep-1993 #text_change 08-Dec-2000

(Species: Ascession: A29081; A94044; A29090; A32739; I51959; I63133; I54011; I68160; A03

(Name, F. Lum, J.B., McGill, A.R.; Moore, C.M.; Naylor, S.L.; van Bragt, P.H.; Baldwin

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A) Title: Human transferrin: CDNA characterization and chromosomal localization.

A) Reference number: A20981; MUID: 84194084; PMID: 6585826
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A/Cross-references: EMBL:M12530; NID:g339452; PIDN:AAA61140.1; PID:g339453
A/Note: the authors translated the codon CAA for residue 203 as Glu
A/Note: the authors translated the codon CAA for residue 203 as Glu
B/A/Cross-reference 2034.353, 1983
A/Ritle: The primary structure of human serum transferrin. The structures of seven cyand
A/Reference number: A92417; MUID:83160878; PMID:6833213
A/Accession: A92417

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A.71tle: Organization of the human transferrin gene: direct evidence that it originated A:Title: Organization of the human transferrin gene: direct evidence that it originated A:Reference number: A94044 MUID:85216459; PMID:3858812
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 73-263, E., 265-328, N/, 330-562 <PAR>
A:Cross-references: EMBL:M1361
B:Adrian, G.S.; Korinek, B.W.; Bowman, B.H.; Yang, F.
A:Title: The human transferrin gene: 5' region contains conserved sequences which match A:Reference number: A29090; MUID:87192006; PMID:3106157
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A.Resdues: 422-690, 'G', 692-698 <UZA>
A.Resdues: 422-690, 'G', 692-698 <UZA>
A.Cross-references: EMBL:M12525; NID:9339468; PIDN:AAA61142.1; PID:9339469
A.Cross-references: EMBL: Mendez, E.; Sinha, S.K.; Sutton, M.R.; Lineback-Zins, J.; Brew, Proc. Natl. Acad. Sci. U.S.A. 79, 2504-2508, 1982
A.Title: The complete amino acid sequence of human serum transferrin.
A.Reference number: A93911; MUID:8222166; PMID:6953407
A.Contents: annotation; disulfide bonds
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                                                                                                                                                         Length 696;
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A; Title: A cloned gene for human transferrin.
A; Reference number: 151959; MUID:92231399; PMID:1809186
A; Accession: I51959
A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                               ; Score 120; DB 1;
; Pred. No. 2.4e-07;
11; Mismatches 14;
F;1-696/Product: transferrin #status predicted <MAT> F;1-335/Domain: transferrin repeat homology <TRH1>
                                                                                                                                                    44.98;
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A; Residues: 1-72; 291-300 <ADR>
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA A; Residues: 1-698 < YAN>
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Matches
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A. Molecule type: protein
A. Residues: 482-515, 'V',517-544 < EVA>
A. Residues: 482-515, 'V',517-544 < EVA>
A. Molecule type: protein
A. Residues: 482-515, 'V',517-544 < EVA>
A. Molecule type: protein
A. Feference number: 326504; MUID:83074540; PMID:6816218
A. Accession: A26504
A. Molecule type: protein
A. Residues: 19-24, 'N',26, 'X',28-29,'S' < HEA>
A. Molecule type: protein; transferrin repeat homology
C. Superfamily: transferrin; transferrin repeat homology
C. Superfamily: transferrin #status experimental < MAT>
F: 19-694/Product: transferrin #status experimental < MAT>
F: 19-549/Domain: transferrin repeat homology < CRRHI>
F: 19-549/Domain: transferrin repeat homology < CRRHI>
F: 27-66,37-57,136-212,155-149,176-192,179-195,189-197,245-259,357-611,363-395,373-386
F: 508/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                      A; Wolecule type: protein
A; Residues: 19-26, XX, 28-36, XX, 38-53 < CHU>
R; Godovac-Zimmermann, J.
Biol. Chem. Hoppe-Seyler 369, 93-96, 1988
A; Title: Isolation, characterization and N-terminal amino-acid sequence of rabbit tra
A; Reference number: $00335; MUID:88209278; PMID:3365331
A; Accession: $00335
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N;Alternate names: lung-derived growth factor; siderophilin
C;Specias: Rattus norvegicus (Norway rat)
C;Date: 16-Eeb-1995 #sequence_revision 12-May-1995 #text_change 20-Aug-1999
C;Accession: S49163; S54980; A30014; A14679; A52389; A30512; I52203
R;Escriva, H.; Pierce, A.; Coddeville, B.; Gonzalez, F.; Benaissa, M.; Leger, D.; Wie submitted to the EMBL Data Library, January 1994
A;Description: Rat mammary gland transferrin: glycan structure, nucleotide sequence a A;Accession: S49163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     serum transferrin and location
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A;Reference number: S54980; MUID:95234054; PMID:7717992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R.Bscriva, H.; Pierce, A.; Coddeville, B.; Gonzalez, F.; Benaissa, M.; Leger, D.;
Blochem. J. 307, 47-55, 1995
                                                                                          Int. J. Blochem. 23, 609-616, 1991
A:Title: Purification of transferrins and lactoferrin using DEAE Affi-Gel Blue.
A:Reference number: A61573; MUID:91293379; PMID:2065820
A:Accession: C61573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Molecule type: protein
A; Residues: 19-45, 'S',47-48, 'Y',50 <GOD>
R; Evans, R.W.; Altken, A.; Patel, K.J.
FEBS. Lett. 238, 39-42, 198
A; Title: Evidence for a single glycan moiety in rabbit s
A; Reference number: $02694; MUID:89005676; PMID:3169252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.4%; Score 110.5; DB 1
llarity 41.7%; Pred. No. 3.8e-06;
Conservative 14; Mismatches 11.
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A;Residues: 1-695 <ESC>
A;Cross-references: EMBL:X77158; NID:9510195;
                                                              S.L.; Shimizu,
                                                              Chung, M.C.M.; Chan, S.L.; Shimi:
it. J. Blochem. 23, 609-616, 1991
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A;Residues: 1-695 <ES2>
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Matches
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A:Molecule type: mRNA
A:Residues: 1-11, 'W',13-50,'I',52-84,'G',86-120,'L',121-130,'I',132-282,'S',284-571,'Q',
A:Cross-references: EMBL:M99209; NID:g164613; PIDN:AA31102.1; PID:g164614
A:Experimental source: mammary gland homology
C;Superfamily: transferrin; transferrin repeat homology
C;Superfamily: transferrin; transferrin repeat homology
C;Superdially: transferrin sequence #status predicted <SIG>F:1-19/Domain: signal sequence #status predicted <SIG>F:20-703/Product: lactoferrin setatus predicted <AMT>
F:20-703/Product: lactoferrin repeat homology <TRH1>
F:36-48/Region: antimiorobial
F:354-69/Domain: transferrin repeat homology <TRH2>
F:36-62,38-53,129-212,171-187,184-195,245-259,362-394,372-385,419-698,439-661,471-546,49
F:77,107,206,527/Painding site: iron (Asp, Tyr, Tyr, His) #status predicted
F:409,447,540,609/Painding site: iron (Asp, Tyr, Tyr, His) #status predicted
F:407/Rainding site: carbonate (Arg) #status predicted
F:400/Binding site: carbonydrate (Asn) (covalent) #status predicted
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C; Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C; Accession: 552107
R; Olan, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Biochim. Biophys. Acta 1243, 25-32, 1995
Biochim. Biophys. Acta 1243, 25-32, 1995
A; Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet A; Reference number: 552107; MuID:95127729; PMID:7827104
A; Accession: 552107
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C;Species: Oryctolagus cuntculus (domestic rabbit)
C;Decies: Oryctolagus cuntculus (domestic rabbit)
C;Accession: S16546; A61239; C61573; S00335; S02694; A26564; S14853
R;Banfield, D.K.; Chow, B.K.C.; Funk, W.D.; Robertson, K.A.; Umelas, T.M.; Woodworth, Biochim. Blophys. Acta 1089, 262-265, 1991
A;Title: The nucleotide sequence of rabbit liver transferrin cDNA.
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A;Accession: A61239
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R;Plerpaoli, W.; Dall'Ara, A.; Yi, C.; Neri, P.; Santucci, A.; Choay, J.
Cell. Immunol. 134, 225-234, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 115; DB 2; I
Pred. No. 6.1e-08;
3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.2%; Score 118; DB 2; 43.5%; Pred. No. 4.3e-07;
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20; Conservative 1
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ilarity 56.7%;
Conservative

    sheep (fragment)

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A Residues: 1-33 <QIA>
C Superfamily: transferri
C Keywords: duplication
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Best Local Similarity
Matches 17; Conserv
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A; Residues: 1-694 <BAN>
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transferrin - Atlantic salmon (fragment)
C;Species: Salmo salar (Atlantic salmon)
C;Species: Salmo salar (Atlantic salmon)
C;Date: 13-58p-1996 #sequence_revision 13-5ep-1996 #text_change 21-Jul-2000
C;Accession: 151350
R;KYingedal, A.M.
Gene 150, 335-339, 1994
A;Title: Characterization of the 5' region of the Atlantic salmon (Salmo salar) trans
A;Reference number: 151350; MUID:95121925; PMID:7821802
A;Accession: 151350
A;Retaus: preliminary; translated from GB/EMBL/DDBJ
A;Retaus: preliminary; translated from GB/EMBL/DDBJ
A;Retaus: preliminary;
A;Molecule type: DNA
A;Residues: 1-64 <KWL)
A;Coss-references: GB:L26909; NID:9598395; PIDN:AAC42221.1; PID:9598396
C;Genetics:
A;Gene: If
A;Introns: 14/1
C;Superfamily: transferrin; transferrin repeat homology
                      R;Yoshinari, K.; Yuasa, K.; Iga, F.; Mimura, A.
Biochim. Biophys. Acta 1010, 28-34, 1989
A;Ittle: A growth-promocting factor for human myeloid leukemia cells from horse serum A;Accession: S02145; MUID:89076897; PMID:2909248
A;Reference number: S02145; MUID:89076897; PMID:2909248
A;Residues: 20-35, X',37, X',37, X',39-40, X',43-44 <YOS>
A;Residues: 20-35, X',37, X'
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C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C; Accession: Til749
Nol. Marine Biol. Biotechnol. 2, 233-238, 1993
A; Tiltle: Cloning and characterization of Atlantic salmon (Salmo salar) serum transfer A; Reference number: 217332; MUID:94122797; PMID:8293074
A; Reference number: 217332; MUID:94122797; PMID:8293074
A; Reference number: 217332; MUID:94120797; PMID:8293074
A; Residues: Til749
A; Residues: 1-690 cKVID
A; Cross-references: EMBL:120313; NID:9431609; PIDN:AAA18838.1; PID:9431610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 VQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: liver
C; Superfamily: transferrin; transferrin repeat homology
C; Reywords: iron binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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Pred. No. 0.0085;
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DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Mismatches
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1 Similarity 32.6%;
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.7%;
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les 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transferrin - Atlantic salmon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best:Local Similarity
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R; Huggenvik, J.I.; Idderda, R.L.; Haywood, L.; Lee, D.C.; McKnight, G.S.; Griswold, M.D. and and confound jilo, 322-340, 1897
A/Title: Transferrin messegor inbourded acid: molecular cloning and hormonal regulation of the confound and program of the confound and hormonal regulation and accession: A30014; MUID:870539; PMID:3023031
A/Reference number: A30014; MUID:870539; PMID:3023031
A/Residues: 518-687, D.Y. A0014; MUID:870539; PMID:3023031
A/Residues: 518-687, D.Y. A0014; MUID:870539; PMID:3023031
A/Reference number: A1001-1029, 1379-ph. A/Residues: 518-687, A/Reference number: A1001-1029, 1379-ph. A/Reference number: A14679; MUID:80049855; PMID:50689
A/Residues: 20-47-5589
A/Residues: 20-47-5589
A/Residues: 20-47-5589; MUID:80049855; PMID:771188
A/Residues: 20-771; A107-77189
A/Residues: 20-705; A107-77189
A/Residues: A005223; A107-8006; PMID:8006; PMID:80069
A/Residues: A00526-64, A107-80069
A/Residues: A00526-64, A107-80
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N.Alternate names: growth-promoting factor
C.Species: Equus caballus (domestic horse)
C.Species: Equus caballus (domestic horse)
C.Bate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
C.Accession: S33761; S02145
R.Carpenter, M.A., Broad, T.E.
Blochim Blophys: Acta 1173, 230-232, 1993
A.Title: The CDNA sequence of horse transferrin.
A.Reference number: S33761; MUID:93277958; PMID:8504171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-706 <CAR>
A;Cross-references: EMBL:M69020; NID:g164242; PIDN:AAA30958.1; PID:g164243
A;Experimental source: liver; developmental stage adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
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C,Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication
F;20-348/Domain: transferrin repeat homology <TRH1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S33761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23
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F;711-738/Pomain: Garboxyl-terminal propeptide #status predicted <CTP>
F;38,135,515/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;710/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Rose, T.M.; Plowman, G.D.; Teplow, D.B.; Dreyer, W.J.; Hellstrom, K.E.; Brown, J.P.
roc. Natl. Acad. Sci. U.S.A. 83, 1261-1265, 1986
Title: Primary structure of the mman melanoma-associated antigen p97 (melanotransferr
;Reference number: A23814; MUID:86149285; PMID:2419904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Construction of the common of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Homo sapiens (man)
Dațe: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 28-Jan-2000
                                                                                                         Gaps
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S
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                                          Pred. No. 0.076;
3; Mismatches 16; Indels
                                                                                                                                                                                                                                                       6 VQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   melanoma-associated antigen gp95/p97
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Pred. No. 0.081;
; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -709/Domain: transferrin repeat homology <TRH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: GDB:119387; OMIM:155750
32.6%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              melanotransferrin precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.7%;
                                    Best Local Similarity 32.6
Matches 14; Conservative
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: A23814
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Gaps

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Indels

366

ò g Search completed: August 11, 2003, 08:18:58 Job time : 14.0485 secs

6 VQWCAVSQPEATKCFQWQRNMRKVR-GPPVSCIKRDSPIQCIQ 47

Conservative

us-09-508-095-19.rsp

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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 11, 2003, 08:16:36; Search time 6.99029 Seconds (without alignments) 322.917 Million cell updates/sec Run on:

US-09-508-095-19 267 1 GRRRSVQWCAVSQPEATKCF.....VRGPPVSCIKRDSPIQCIQA 48 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

127863 seqs, 47026705 residues

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	ı O	07/011 equus cabal		_		pos			Ollott	Sus			DID346 retting norm		P79815 oncorhynchu					_	P02789 gallus qali		P79819 oryzias lat		٠.	_	_	Q92079 gadus morhu		P34692 caenorhabdi	. Q00999 herpesvirus
SUMMARIES	TRFL_HUMAN	TRFL CAPHI	TRFL_CAMDR	TRFL_MOUSE	TRFL_BUBBU	TRFL_BOVIN	ICA_PIG	TREE_PIG	TOTAL PLANT	TOPE BONTN	TREE PARTY	TREE MOUSE	TRFE RAT	TRFE HORSE	TRFE_ONCKI	TRFE_ANAPL	TRF1_SALSA	TRF2_SALSA	TRFM_HUMAN	TRFE_PAROL	TRFE_CHICK	TRFM_MOUSE	TRFE_ORYLA	SAX_RANCA	TRFE_XENLA	TYRA_ERWHE	YTE4_CAEEL	TRFE_GADMO	FAS_RAT	U183_CAEEL	VCAP_HSVSA
Length DB	711 1				708 1		T 000	1 6 6 6	70,4	704	695	697	698 1	706 1	687 1	686 1	690 1	691 1	738 1	685 1	705 1	738 1		844 1	•		546 1	642 1	2505 1	422 1	1371 1
& Ouery Match Le	97.8	61.0	60.7	59.6	50.0	20.7	0.4	44.9	. 4	; _	; ;	. 6		38.6	32.0	29.0	28.7	28.7	28.7	28.5	28.5	28.3	27.5	27.3			21.3	21.3		20.2	20.0
Score	261	163	162	159	136	134	136.0	118.5	118	112	110.5	106.5	106.5	103	85.5	77.5	76.5	76.5	76.5	16	76	75.5	73.5	73	72	57	57	57	25		53.5
Result No.	17	ĸ	4	in '	9 1	~ a	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	97	. 27	28	57	30	31	32	33

Q9h112 homo sapien P07023 escherichia O97046 capra hircu Q60837 mus musculu Q9de13 gailus gall O24006 i antimicro P22297 manduca sex Q9778 schizosacch Q64331 mus musculu Q83485 tobamovirus P08564 rubella vir P18627 homo sapien
CS11_HUMAN TYRA_ECOLI BD01_CAPHI 112R_MOUSE BA2B_CHICK MAP_IMBBA TRF_MANSE SYO_SCHPO MYO6_MOUSE MOVP_TMOB POLS_RUBV LAG3_HUMAN
нананданана -
137 64 64 738 2130 333 681 1265 274 522 525
0.0011 0.0011 0.0010 0.
53 52.5 52.5 52.5 51.5 51.5 51.5 50.5
33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3

# ALIGNMENTS

RESULT 1

TRFL_H ID T	UMAN RFL_HUMAN STANDARD;
AC A	000756;
S E	Q9H123; 21-JUL-1986 (Rel. 01, Created)
DI	38,
DŢ	(Rel. 42, Last
四日	Ω,
E C	Lactoferroxin B; Lactoferroxin C].
SO	Homo sapiens (Human)
88	
ပ္ပ	Sutheria; Primates;
XO	)=9606;
Ä	[1]
RP	SEQUENCE FROM N.A.
2 Z	TISSUE-Mammary gland; MEDITME-00204020, Bubwed-24024EE
RA R	402403;
2	"Complete Ducleotide sequence of human mammary aland lactoferrin ".
RL	leic Acids Res. 18:5288-5288(1990).
RN	[2]
RP	
S :	TISSUE=Mammary gland;
KA	
R.L.	Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea
X C	[5]
4 6	SECTION N. P.
KA F	).M.;
7 Z	Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
2 0	( to ) Condition of the
7 C	SECUENCE FROM N.A.
ž,	TISSUE=Manmary gland;
¥ E	Liang U., Jimenez-Flores R., Richardson T.;
H.	"Molecular cloning and sequence analysis of human lactoferrin.";
7 2	<pre>Lubmitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.</pre>
S C	101
ች ር ቻ ር	MEDUCANCE FROM N.A.
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7 Z	John Leed (FEB-1994) to the EMBL/Genbank/DDBJ databases. [6]
A A	COLINGE PROM N A
RC	TISSUE-Mammary gland:
RA	Cheng H., Chen X., Huan L.;
RT	"cDNA cloning and sequence analysis of human lactoferrin ".
RL	EMBL/GenBank/DDBJ databases.
N.	[7]
RP	SEQUENCE FROM N.A.
Σ.	TISSUE=Prostate;
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¥.	ouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

us-09-508-095-19.rsp

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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzratne P.H.,
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Altinalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Aniting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.;
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McComble W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,

Nhan M., Parnell L., Dedhia N., Ansarl A., Mardis E., Schutz K.,

Gnoj L., la Bastida M., Kablan N., Greco T., Touchman J., Muzny D.,

Chen C.N. Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,

Dragan Y., Glacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,

Dlaz-Perez S., Zhou X., Yu Y., Matanabe M., Doggett N., Garcia D.,

Sagripanti J.L.,
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Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
"Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
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MEDLINE-82046817; PubMed-6794640;
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 609-711.
MEDLINE-52262043; PubMed-7049727;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
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MEDLINE-88001031; PubMed-3477300;
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"Isolation of lactoferrin cDNA from a human myeloid library and expression of manA during normal and leukemic myelopolesis.";
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MEDLINE=85076667; PubMed=6510420;

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"Human lactotransferrin: amino acid sequence and structural comparisons with other transferrins.";

Eur. J. Biochem. 145:659-666(1984).
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Nucleic Acids Res. 18:4013-4013(1990).
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MEDLINE-90326549; PubMed-2374734;
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AEDLINE-99091914; PubMed-9873069;

AEDLINE-99091914; PubMed-9873069;

RA Kilthworth G.K., Sommer J.R., Obritan G., Han L., Ahmed M.N.,

A Qumsiyeh M.B., Lin P.-Y. Basti S., Reddy M.K., Kanai A., Hotta Y.,

A Quar J., Kunaramanickavel G., Munier F., Schorderet D.F.,

RA Hejtmancik J.F., Teng C.T.;

A Hejtmancik J.F., Teng C.T.;

RT Familial subepithelial corneal amyloidosis (gelatinous drop-like corneal dystrophy): exclusion of linkage to lactoferrin gene.";

RT Corneal dystrophy): exclusion of linkage to lactoferrin gene.";

RT Corneal dystrophy): exclusion of linkage to lactoferrin gene.";

RT Corneal dystrophy): exclusion of linkage to lactoferrin gene.";

RO Vision 4:31-32(1999).

C -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING CC OF AN ANTON, USUALLY BICARBONATE.

C -!- FUNCTION: LACTOFERROXINS A, B AND C HAVE OPIOID ANTAGONIST ACTIVITY. LACTOFERROXINS A, B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE CC FOR KAPPA-RECEPTORS. THAN FOR MU-RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91166929; PubMed-1369293;
Tani F., Ilo K., Chiba H., Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived
from human lactofarratin.";
Agric. Biol. Chem. 54:1803-1810(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE-99192677; PubMed-10089508;
Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
"Structure of human apolactoferrin at 2.0-A resolution. Refinement
and analysis of ligand-induced conformational change.";
Acta Crystallogr. D 54:1319-1335(1998).
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                                                                                                                                                                                                                                                     "Mutagenesis of the histidine ligand in human lactoferrin: iron binding properties and crystal structure of the histidine-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- DOMAIN: COMPOSED OF TWO HOWOLOGOUS DOMAINS.
-i- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                            Haridas M., Anderson B.F., Baker E.N.; "Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                    OF 20-353.
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                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS)
                  [15]
X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
                                                                                                                         Acta Crystallogr. D 51:629-646(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION OF LACTOFERROXINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Secreted.
Mol. Biol. 209:711-734(1989).
                                                                                                                                                                                                                                                                                         253-->methionine mutant.";
Biochemistry 36:341-346(1997).
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AAA36159.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
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PROSITE; PS00205; TRANSFERRIN_1; 2.
PROSITE; PS00206; TRANSFERRIN_2; 2.
PROSITE; PS00207; TRANSFERRIN_3; 1.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat; Signal; 3D-structure.
                                                                                         ;
               ch 97.8%; Score 261; DB 1; Length 711;
1 Similarity 100.0%; Pred. No. 3.7e-26;
47; Conservative 0; Mismatches 0; Indels
                                                                                                                                            2 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA 48
                                                                                                                                                                        22 RRRSVQWCAVSQPEATKCFQWQRNWRKVRGPPVSCIKRDSPIQCIQA 68
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Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
"CDNA sequence of mare lactoferrin.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                           15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LACTOTRANSFERRIN.
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PDB; 1B7V; 02-FEB-99.
PDB; 1B7Z; 02-FEB-99.
PDB; 1F9B; 10-FEB-01.
PDB; 116B; 13-FEB-02.
PDB; 1QJM; 14-JAN-00.
InterPro; 1PR001156; Transferrin.
Pfam; PF00405; transferrin.
PRINTS; PR00422; TRANSFERRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99296631; PubMed-10366507;
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                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                  Best Local Similarity
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077811;
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TRFL_HORSE
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                                                                                                                                                                                                                                                                                                                                                                            Le Provost F., Nocart M., Guerin G., Martin P.;
"Characterization of the goat lactoferrin cDNA. Assignment of the relevant locus to bowine U12 synteny group.",
Blochem. Blophys. Res. Commun. 203:1314-1332(1994).
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH OA BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUBALLY BICARRENDATE.
-!- SUBGELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                          Capra hircus (Goat).
Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
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Pfam; PF00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR_FER; 2.
PROSITE; PS00205; TRANSFERRIN_1; 2.
PROSITE; PS00206; TRANSFERRIN_2; 2.
PROSITE; PS00207; TRANSFERRIN_3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
   9 RKSVRWCTISPAEAAKCAKFQRNMKKVRGPSVSCIRKTSSFECIQA 54
                                                                                                                                                                                                                                                                           TISSUE-Mammary gland;
Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                15-DEC-1998 (Rel. 37, Last Sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin)
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MEDLINE=94380047; PubMed=8093048;
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last seq
28-FEB-2003 (Rel. 41, Last ann
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HSSP; 077698; 1CE2.
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Pred. No. 1.2e-13;
9; Mismatches 9; Indels
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60.9%;
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nes 28; Conservative
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                                                                                                 EMBL; AJ111674; CAB53387.1; -.

REMBL; AJ111674; CAB53387.1; -.

REMBL; AF168879; AAF82241.1; -.

REMBL; DTZ; 20-UNN-01.

InterPro; IPR001156; Transferrin, 2.

REMART; SMO0049; TRANSFERRIN.

RART; SMO0094; TRANSFERRIN.

REMOSITE; PS00206; TRANSFERRIN.

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REMOSITE PS002
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A -> Q (IN REF. 2).
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Matches 26; Conservative
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
NCBI_raxID-9838;
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STRANI"-Somall; TISSUE-Lactating mammary gland;
STRAPINE S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486(1999).
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16-007-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Lactotransferrin precursor (Lactoferrin).
                                                                                      SIMILARITY
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A SEQUENCE FROM N.A.

A STRANSPET R.L., FeIngold E.A., Grouse L.H., Derge J.G.,

RA Altasner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapteton M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hilyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,

RA Pillalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Schentz J., Lu X., Smailus D.E.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length
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"Characterization of estrogen-responsive mouse lactoferrin promoter.";
"Characterization of estrogen-responsive mouse lactoferrin promoter.";
J. Biol. Chem. 266:21880-21885(1991).
- !- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                       Pentecost B.T., Teng C.T.;
"Lactotransferrin is the major estrogen inducible protein of mouse
                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Lactotransferrin precursor (Lactoferrin).
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J. Biol. Chem. 262:10134-10139(1987).
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MEDLINE-92042099; PubMed-1939212;
                                                                                                                                                                                                                                                                                              MEDLINE-87280033; PubMed-3611056;
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InterPro; IPR001156; Transferrin.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bubalus.
NCBI_TaxID=89462;
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MR -> IQG (IN REF. 1).
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IRON 2 (BY SIMILARITY).
ANION (POTENTIAL).
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S -> T (IN REF. 2).
S -> T (IN REF. 1).
A -> D (IN REF. 1).
E -> G (IN REF. 1).
L -> V (IN REF. 1).
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Pred. No. 5.5e-13;
                                                                                                          LACTOTRANSFERRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Lactotransferrin precursor (Lactoferrin)
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BY SIMILARITY.
Pfam; PF00405; transferin; 2.
PRINTS; PR00422; TRANSFERIN.
SMART; SM00094; TR_FER; 2.
PROSITE; PS00205; TRANSFERIN_1; 1.
PROSITE; PS00206; TRANSFERRIN_2; 2.
PROSITE; PS00207; TRANSFERRIN_3; 2.
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                                                                                             NEDLINE-20003130; PubMed=10531476; MEDLINE-20003130; PubMed=10531476; MEDLINE-20003130; PubMed=10531476; MEDLINE-20003130; PubMed=10531476; MEDLINE-20003130; PubMed=10531476; Medline S., Stington S., Paramasivam M., Yadav S., Stinivasan A., Singh T.P.; Structure of buffallo lactoferrin at 2.5-A resolution using crystals grown at 303 K shows different orientations of the N and C lobes."; Acta Crystallogr. D SS:1805-1813(1999).

-I-FUNCTION: TRANSFERRING ARE IRON BINDING TRANSPORT PROTEINS WHICH ON BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USGUALLY BICARBONATE.
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R PDB; 1CE2; 19-MAR-99.

R DBS; 1BIY; 13-JAN-99.

R InterPro; 1PR001156; Transferrin.

R Pfam; PF00405; transferrin; 2.

R PRINTS; PR00422; TRANSFERRIN.

R SMART; SM00094; TRANSFERRIN.

R PROSITE; PS00206; TRANSFERRIN.

R PROSITE; PS00207; TRANSFERRIN.

R TRANSPORT; Iron transport; Glycoprotein; Metal-binding; Repeat;

R Signal, 3D-structure.
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. .) (POTENTIAL).
SEQUENCE FROM N.A.
Paramasivam M., Thattallyath B.D., Kumar A., Srinivasan A.,
Singh T.P.,
"CDNA sequence of Buffalo lactoferrin.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                               -!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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                                                                                                                                                                                       SEQUENCE FROM N.A.

TISSUE-Blood, and Mammary gland;
MEDLINE-94266164; Pubmed-8206385;
Seyfert H.-M., Tuckoricz A., Interthal H., Koczan D., Hobom G.;
"Structure of the bovine lactoferrin-encoding gene and its promoter.";
Gene 143:265-269(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98190007; PubMed-9521752;

Hwang P.M., Zhou N., Shan X., Arrowsmith C.H., Vogel H.J.;

Hwang P.M., Zhou N., Shan X., Arrowsmith C.H., Vogel H.J.;

Hwang P.M., Zhou N., Shan X., Arrowsmith C.H., Vogel H.J.;

Hydrae-dimensional solution structure of lactoferzioin B, an antimicroblal peptide derived from bovine lactoferzioin.";

Biochemistry 37:4288-4298(1998).

-I-FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANYON, USUALLY BICARBONATE.

-I-FUNCTION: LACTOFERRICIN B IS AN ANTIMICROBIAL PEPTIDE.
                                                                                                                 TISSUB-Lung;
Trang T.C., Burns D.K., Wang F., Pan Y.C.E., Schmidt A.M., Stern D.;
"Cloning of a 80-kD advanced glycosylation end product (AGE) binding
Protein from bovine lung.";
PASEB J. 6:233-233(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98062367; PubMed-9398529;
Moore S.A., Anderson B.F., Groom C.R., Haridas M., Baker E.N.;
"Three-dimensional structure of diferric bovine lactoferrin at 2.8-A
                                    MEDITNE-92028986; PubMed-1718281;
Goodman R.E., Schanbacher F.L.;
"Bovine lactoferrin mRNA: sequence, analysis, and expression in the
                                                                                                                                                                                                                                                                                                                                         Rejman J.J., Hegarty H.M., Hurley W.L.;
"Purification and characterization of bovine lactoferrin from secretions of the involuting mammary gland: identification of multiple molecular weight forms.";
Comp. Biochem. Physiol. 93B:929-934(1989).
                                                                                                                                                                                                                                                                                Nakamura I., Shimazaki K., Yagi Y., Watanabe A.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                    Biochem. Biophys. Res. Commun. 180:75-84(1991).
                                                                                                                                                                                                                                                                                                                                                                                                             K-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
   Biochem. 196:177-184(1991)
                                                                                                                                                                                                                                                                                                                              MEDLINE-90031466; PubMed-2805645;
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AAA21722.1;
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AAA21722.1;
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                          SEQUENCE FROM N.A.
                                                                                                          SEQUENCE FROM N.A.
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                                                                         mammary gland.";
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MEDLINE-91160550; PubMed-2001696;
Pierce A., Colavizza D., Benaissa M., Maes P., Tartar A.,
Montreuil J., Spik G.;
"Molecular cloning and sequence analysis of bovine lactotransferrin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P24627; Q29629; Q9MXY3; O1-WAR-1992 (Rel. 21, Created) O1-CT-1993 (Rel. 27, Last sequence update) CT-1993 (Rel. 27, Last sequence update) Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferricin (LFCIN B)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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Pred. No. 5.2e-10;
14; Mismatches 12;
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Best Local Similarity
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NCBI_TaxID-9913;
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-97254619; PubMed-9100029;
Webbens M.W., Roush E.D., Decastro C.M., Fierke C.A.;
"Cloning, sequencing, and recombinant expression of the porcine inhibitor of carbonic anhydrase: a novel member of the transferrin family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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MEDLINE=93099129; PubMed=1463741;
Roush B.D., Fierke C.A.;
Purification and characterization of a carbonic anhydrase II
Inhibitor from porcine plasma.";
Biochemistry 31:12536-12542(1992).
-! FUNCTION: SPECIFICALLY BINDS AND INHIBITS CARBONIC ANHYDRASE
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Inhibitor of carbonic anhydrase precursor.
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Best Local Similarity 43.5%;
Matches 20; Conservative
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EMBL: L19986; AAA21722.1; JOINED.
DR EMBL: L19986; AAA21722.1; JOINED.
DR EMBL: L19989; AAA21722.1; JOINED.
DR EMBL: L19999; AAA21722.1; JOINED.
DR EMBL: L19991; AAA21722.1; JOINED.
DR EMBL: L19991; AAA21722.1; JOINED.
DR EMBL: AB046664; BAB03470.1; -.
DR EMBL: AB046664; BAB03470.1; -.
DR PDB; ILFC: 18-NOV-98.
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N-LINKED (GLCNAC...).
/*TIG-CAR_00186.
N-LINKED (GLCNAC...).
/*TIG-CAR_00197.
N-LINKED (GLCNAC...).
/*TIG-CAR_00197.
/*TIG-CAR_00198.
E -> A (IN REF. 4).
E -> PQ (IN REF. 4).
C -> PQ (IN REF. 1).
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                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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"Nucleotide sequence of porcine liver transferrin.";

Nucleic Acids Res. 16:8720-8720(1988).

!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USBALLY BICARBONATE. IT IS RESPONSIBLE FOR THE
TRANSPORT OF IRON FROM STIES OF ABSORPTION AND HEME DEGRADATION
TO THOSE OF STORAGE AND UTILIZATION. SERUM TRANSFERRIN MAY ALSO
HAVE A FURTHER ROLE IN STIMULATING CELL PROLIFERATION.
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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01-FEB-1991 (Rel. 17, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Serotransferrin (Transferrin) (Siderophilin) (Beta-1-metal binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBL_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
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TISSUE SPECIFICITY: Expressed in liver; secreted in plasma.
DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                            3 RRSVQWCAVSQPEATKCFQWQRNMRK---VRGPPVSCIKRDSPIQCIQA 48
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                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 704;
                                                                                                                                                                                                                                                                                                                   INHIBITOR OF CARBONIC ANHYDRASE
                                                                                                                                                                                                                                                                                                                                                             49.6%; Score 132.5; DB 1; Length 49.0%; Pred. No. 1.5e-09; tive 11; Mismatches 11; Indels
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                                                         -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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                                                                                                                                                                                                                                                                                                        POTENTIAL.
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                                                                                                                                                                                                       InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 2.
PRINTS; PR00421; TRANSFERRIN.
SMART; SM00094; TR_FER; 2.
PROSITE; PS00205; TRANSFERRIN_1; 2.
PROSITE; PS00206; TRANSFERRIN_2; 1.
PROSITE; PS00207; TRANSFERRIN_2; 1.
                       SUBCELLULAR LOCATION: Secreted. TISSUE SPECIFICITY: Plasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                        EMBL; U36916; AAB58956.1; -. PIR; I47228; I47228.
  NANOMOLAR AFFINITY
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 49.0 tes 24; Conservative
                                               PTM: N-GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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704 AA;
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P09571;
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P027787, O43890; O9ND88; Q9UHVO;
21-UUL-1986 (Rel. 01, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal binding globulin) (FRO1400).
                                                                                                                                                                             PIR; S01384; S01384.
PDB; 1H76; 15-JAN-02.
InterPro; IRRO01156; Transferrin.
Pfam; PF00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR_FER; 2.
PROSITE; PS00205; TRANSFERRIN.1; 2.
PROSITE; PS00206; TRANSFERRIN.2; 2.
PROSITE; PS00207; TRANSFERRIN.2; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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Best Local Similarity 43.8
Matches 21; Conservative
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Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
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Lineback-Zins J., Brew K.,
"The primary structure of human serum transferrin. The structures of
Seven cyangen bromide fragments and the assembly of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Organization of the human transferrin gene: direct evidence that it originated by gene duplication.":
                                                                                                                                                                                                                            [2] SEQUENCE FROM N.A.
MEDIJNE-88056305; PubMed-3678832;
Schaeffer E., Lucero M.A., Jeltsch J.-M., Py M.-C., Levin M.J.,
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analogous chicken gene and human pseudogene.";
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                                    Craniata, Vertebrata, Euteleostomi,
Catarrhini; Hominidae, Homo.
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BEDLINE-SC16459; Pubmed=3858812;
Park I., Schaeffer E., Sidoli A., Baralle F.E., Cohen G.N.,
Zakin M.M.;
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MEDLINE-87066744; PubMed-3786138;
              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                     NCBI_TaxID=9606;
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Lyndon J.P., O
Conneely O.M.;
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                                                                                                 X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 23-352.
MEDLINE-9915527; PubMed-10029548;
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"Human transferrin G2775 mutation: a risk factor for iron deficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                       LINGUICE CONFORMATIONAL CHANGE IN transferrins: crystal structure of the open form of the N-terminal half-molecule of human transferrin.";
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                           Evans P., Kemp J.;
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                                                                                                                                                                                                                                                                                                Pang H., Koda Y., Soejima M., Kimura H.;
"Identification of a mutation (A1879G) of transferrin from cDNA
prepared from peripheral blood cells.";
Ann. Hum. Genet. 62:271-274(1998).
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         MEDLINE-98434369; PubMed-9760232; Weffrey D., Bewley M.C., Macgillluray R.T.A., Mason A.B., Woodworth R.C., Baker B.N.; Ligand-induced conformational change in transferrins: crys!
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 X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TREL_PIG STANDARD; PRT; 704 AA. P14632; 029557; 01-APR-1990 (Rel. 14, Created) 2-DEC-1998 (Rel. 37, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
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                                                                            31ochemistry 37:13978-13986(1998).
                                                                                                                                                                                                      VARÍANT SER-142.
MEDLINE-98019079; PubMed-9358047;
                                                                                                                                                                                                                                                                                  MEDLINE-99020112; PubMed-9803271;
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MEDLINE-92379101; Pubmed-1511016;
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22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-90105538; PubMed-2605266; Hutchens T.W., Magnuson J.S., Yip T.-T.; Hutchens T.W., Magnuson J.S., Yip T.-T.; Magnuson J.S., Zip T.-T.; Magnuson J.S., Zip T.-T.; Magnuson J.S., Mag
                                                                                               "Nucleotide and primary amino acid sequence of porcine lactoferrin."; Biochim. Biophys. Acta 1132:97-99(1992).
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O'Malley B.R., Saucedo O., Lee T., Headon D.R.,
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Alexander L.J., Levine W.B., Teng C.T., Beattle C.W.;
"Cloning and aequencing of the porcine lactoferrin cDNA.";
Anim. Genet. 23:251-256(1992).
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Pfam; PF00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SMO094; TR_FER; 2.
PROSITE; PS00205; TRANSFERRIN_1; 2.
PROSITE; PS00206; TRANSFERRIN_2; 2.
PROSITE; PS00207; TRANSFERRIN_2; 1.
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-!- SUBCELLULAR LOCATION: Secreted
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HSSP; O77698; 1CE2.
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HSSP; P19134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. BIOL. Chem. 271:1166-1173(1996).

-1 FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FEREIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE. IT IS RESPONSIBLE FOR THE TRANSPORT OF IRON FROM SITES OF ABSORPTION AND HEME DEGRADATION TO THOSE OF STORAGE AND OTILIZATION. SERUM TRANSFERRIN MAY ALSO HAVE A FURTHER ROLE IN STIMULAFING CELL PROLIFERATION.
-1 SUBJUNIT: MONOMER (By similarity).
-1 SUBCELLUTAR LOCATION: Secreted.
-1 ILSSUE SPECIFICITY: Expressed in liver; secreted in plasma.
-1 DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-1 SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                           N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
G -> W (IN REF. 1).
RRT -> TTR (IN REF. 3).
M -> I (IN REF. 1).
D -> G (IN REF. 1).
MISSING (IN REF. 2).
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93261EFD608AD358 CRC64;
    SIMILARITY).
              ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   binding globulin).
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P19134; Od514;
01-NOV-1990 (Rel. 16, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal binding globulin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-91274362; Pubmed-2054387;
Banfield D.K., Chow B.K.-C., Funk W.D., Robertson K.A., Umelas T.M.,
Woodworth R.C., Macgillivray R.T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                    Iron transport; Glycoprotein; Metal-binding; Repeat;
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IRON 2 (BY SIMILARITY).
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SEROTRANSFERRIN
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12; Mismatches
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Interpro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
PROSITE; PS00205; TRANSFERRIN_1; 1.
PROSITE; PS00206; TRANSFERRIN_2; 2.
PROSITE; PS00207; TRANSFERRIN_3; 1.
Transport; Iron transport; Glycoprote
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704 AA;
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DDB; 1TFD; 15-ARR-93

PDB; 1TFD; 15-ARR-92

InterPro; 1FR001156; Transferrin.

Pfam; PF00405; transferrin. 2.

PRINTS; PR00422; TRANSFERRIN. 2.

PROSTIE; PS00206; TRANSFERRIN. 1; 1.

PROSTIE; PS00206; TRANSFERRIN. 2; 2.

PROSTIE; PS00206; TRANSFERRIN. 2; 2.

PROSTIE; PS00206; TRANSFERRIN. 3; 2.

Transport; Inton transport; Glycoprotein; Metal-binding; Repeat; Signal; 3D-structure.
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IRON 1 (BY SIMILARITY)
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IRON 1 (BY SIMILARITY)
IRON 2 (BY SIMILARITY)
ANION (POTENTIAL).
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MISSING (IN REF. 1).
K -> S (IN REF. 3).
P -> Y (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89026775; PubMed-3179277;
Balley S., Evans R.W., Garratt R.C., Gorinsky B., Hasnain S.,
Horsburgh C., Jhoti H., Lindley P.F., Mydin A., Sarra R., Watson J.L.;
"Molecular structure of serum transferrin at 3.3-A resolution.";
Biochemistry 27:5804-5812(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                     'Cloning and stuctural organisation of the rabbit transferrin encoding
                                                                                                                                                                                                                                                               Evans R.W., Aitken A., Patel K.J.;
"Evidence for a single glycan moiety in rabbit serum transferrin and location of the glycan within the polypeptide chain.";
FEBS Lett. 238:39-42(1988)
                                                                                                                                          SEQUENCE OF 20-51.
MEDLINE-88209278; PubMed-3365331;
Godovac Zimmermann J.;
"Isolation, characterization and N-terminal amino-acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Monomer.
SUBCELLUIAR LOCATION: Secreted.
TISSUE SPECIFICITY: Expressed in liver; secreted in plasma.
DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
"The nucleotide sequence of rabbit liver transferrin cDNA.";
Blochim. Biophys. Acta 1089:262-265(1991).
                                    SEQUENCE FROM N.A.
STRAIN-New Zealand white;
Ghareeb B.A.A., Thepot D., Puissant C., Cajero-Juaerez M.
Hondebine L.A.
                                                                                                               Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                           Biol. Chem. Hoppe-Seyler 369:93-96(1988).
                                                                                                                                                                                                                                                                                                                                  -RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
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AF031611; AAB94136.1;
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AAB94136.1;
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AAB94136.1;
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AAB94136.1
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                                                                                                                                                                                                rabbit transferrin.
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                       15-SEP-2003 (Rel. 41, Last sequence update)
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal TF OR TRF.
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_raxID=10090;
                                                                                                                                                                                                                                                                                                                                 TRFE_MOUSE STANDARD; PRT; 697 AA.
Q921111: 035421; Q61803; Q62358; Q62359; Q63915; Q64515; Q8VII5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lai D.-Z.; "Construction of a robust CHO cell-line for biopharmaceutical
                                                                                                                                                                                                                                   Length 695;
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                  76670 MW; DB12F34D87AE9D55 CRC64;
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                                                                                                                                                                                                                                                   14; Mismatches
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28-FEB-2003 (Rel. 41, Last seq
15-SEP-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                   41.48;
41.78;
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Matches 20; Conserv
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SEQUENCE FROM N.A.
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transferrin promoter in Sertoli
            Sanchez A.,
G.G.,
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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schmer A., Schmitz J., Myers R.M., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Transferrin mRNA level in the mouse mammary gland is regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kasik J.W., Rice E.J.;
"Transferrin gene expression in maternal liver, fetal liver and
placenta during preparancy in the mouse.";
Placenta 14:365-371(1993).
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SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Expressed in liver; secreted in plasma.
DOMAIN: COMPOSED OF TWO HONOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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MEDLINE-88086992; PubMed-3693348;
Chen L.-H., Bissell M.J.;
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MGD; MGI:98821; Trf.
GO; GO:0030139; C:endocytic vesicle; IDA.
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98284323; PubMed-9621303;
Chaudhary J., Skinner M.K.;
"Comparative sequence analysis of the
promoters: hormonal regulation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pregnancy and extracellular matrix.", J. Biol. Chem. 262:17247-17250(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 268-307 FROM N.A.
TISSUE-Placenta;
MEDLINE-94068311; PubMed-8248032;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID-10116;
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P12346; Q64628; Q64630;
01-OCT-1989 (Rel. 12, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal binding globulin).
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LT -> FA (IN REF. 1).
ISAS -> HASG (IN REF. 2; AAH08559).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   InterPro; IPR001156; Transferrin.
Prim; PR00405; transferrin. 2.
PRINTS; PR00422; TRANSFERRIN.
PROSITE; PS00206; TRANSFERRIN. 1; 1.
PROSITE; PS00206; TRANSFERRIN. 2; 2.
PROSITE; PS00207; TRANSFERRIN. 3; 2.
Transfport; Iron transport; Glycoprotein; Metal-binding; Repeat; Signal.
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G -> C (IN REF. 4).
A -> D (IN REF. 4).
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H -> S (IN REF. 1).
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MEDILINE-87053639; PubMed-3023031;
Huggenvik J.I., Idzerda R.L., Haywood L., Lee D.C., McKnight G.S.,
Griswold M.D.;
                                                                                                                                                                                                                                                                                                                                        Escriva H., Pierce A., Coddeville B., Gonzalez F., Benaissa M., Leger D., Wieruszeski J.M., Spik G., Pamblanco M.; Rat mammary-gland transferrin: nucleotide sequence, phylogenetic analysis and glycan structure."; Blochem. J. 307:47-55(1995).
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"The synthesis and secretion of rat transferrin.";
J. Biol. Chem. 254:12013-12019(1979).
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-1. SUBCELLULAR LOCATION: Secreted.
-1. TISSUE SPECIFICITY: Expressed in liver; secreted in plasma.
-1. DOMALN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-1. SIMILARITY: BELONGS TO THE TRANSFERRIN PAMILY.
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SEQUENCE FROM N.A.
STRAIN-WASTAIT IISSUE-Liver;
STRAIN-WASTAIT IISSUE-Liver;
MEDLINE-96208933;
Hosino A., Hisayasu S., Shimada T.;
"Complete sequence analysis of rat transferrin and expression
transferrin but not lactoferrin in the digestive glands.";
Comp. Blochem. Physiol. 113B:491-497(1996).
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STRAIN-Wistar; TISSUE-Mammary gland;
MEDLINE-95234054; PubMed-7717992;
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EMBL; X77158; CAA54403.1; -.
EMBL; M27966; AAA4267.1; -.
PIR; S49163; S49163.
HSSP; P19134; 17FD.
Glycosultebb; P12346; -.
InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 2.
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PROSITE; PS00205; TRANSFERRIN.; 1.
PROSITE; PS00206; TRANSFERRIN.; 2.
PROSITE; PS00207; TRANSFERRIN.; 2.
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MEDLINE-80049855; PubMed-500689;
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39.9%; Score 106.5; DB 1; Length 698;
Best Local Similarity 41.7%; Pred. No. 3.3e-06;
Matches 20; Conservative 13; Mismatches 12; Indels 3
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E -> D (IN REF. 4).
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W; DDF2C1918E2A1B0E CRC64;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                 Title:
Perfect score:
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                                                                             OM protein
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oncorhynchu salvelinus paralichthy salmo trutt salmo trutt salmo trutt

Q9PT57 Q918Q9 Q918Q9 Q91A82 Q8AUQ1 Q8AUQ1 Q8AUQ0 Q8AUQ0

salmo trutt oncorhynchu oncorhynchu oncorhynchu

ALIGNMENTS

SUMMARIES			Description	081x02 homo sapien	O8izh6 homo sapien	081u92 homo sapien	08tcd2 homo sapien	O8cba0 mus musculu	Q9ucy5 homo sapien	O8wmn8 sus scrofa	09tr80 ovis aries	Ogdbd0 mus musculu	Q8vc96 mus musculu	09tqv7 equus cabal	09xt72 trichosurus	063602 rattus norv	O9pt13 oncorhynchu	Q8uuk7 oncorhynchu	Ogpu08 oncorhynchu
		•	ID	Q8IX02	0812н6	081092	Q8TCD2	Q8CBA0	Q9UCY5	Q8WMN8	Q9TR80	Q9DBD0	Q8VC96	Q9TQV7	Q9XT72	063602	Q9PT13	Q8UUK7	Q9PU08
			DB	4	4	4	4	Ξ	4	9	9	11	11	9	9	11	13	13	13
	æ		Length	234	711	711	711	707	38	704	33	700	100	54	711	87	691	517	672
	æ	Query	Match	97.8	95.1	95.1	94.8	61.0	54.1	44.9	43.1	42.1	39.9	38.6	37.8	34.6	32.4	32.0	32.0
			Score	261	254	254	253	163	144.5	120	115	112.5	106.5	103	101	92.5	86.5	85.5	85.5
	;	Result	No.		7	m	4	5	9	7	œ	თ	10	11	12	13	14	15	16

Created) Last sequence update) Last annotation update)

01-MAR-2003 (TrEMBLrel. 2 01-MAR-2003 (TrEMBLrel. 2 01-MAR-2003 (TrEMBLrel. 2 Lactoferrin. Homo sapiens (Human).

711 AA.

PRT;

PRELIMINARY;

Q812H6 Q812H6;

Euteleostom1;

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A Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

L Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

- I- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROFIEINS WHICH

CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING

C - I- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

DR RABL; GGO2347; AAR12347.1; -.

DR FOROITS: PROMO156; Transferrin.

DR PROSITE; PS00205; TRANSFERRIN.2; 2.

DR PROSITE; PS00206; TRANSFERRIN.2; 2.

DR PROSITE; PS00206; TRANSFERRIN.3; 2.

DR PROSITE; PS00207; TRANSFERRIN.3; 2.

KW Glycoprotein; Iron transport; Metal-binding; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactotransferrin.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.8%; Score 253; DB 4; Length 711; 97.9%; Pred. No. 4.3e-27; 1ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Butele
Primates; Catarrhini; Hominidae; Homo.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Best Local Similarity 63.6
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                      Eukaryota; Metazoa;
                                          Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                      Mammalia; Euther:
NCBI_TaxID=9606;
                                                                                                                  TISSUE-Prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46;
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                    à
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                                                                                           Kaplan J.B., Fine D.H., "Characterization of an amino acid polymorphism in the antibacterial "Characterization of an amino acid polymorphism in the antibacterial submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AX137470; AAN1304.1; -547AB9423C27CE67 CRC64;
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
      Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Shi Y.-Q., Zhang Y., Zheng Y.-M.;
"Homo sapiens Lactotransferrin Gene: CDNA Cloning and Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUB-Seminal vesicle;
Baskar Singh S., Saravanan K., Paramasivam M., Srinivasan A.,
                                                                                                                                                                                                                                                                                                                                      Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 254; DB 4; Length 711;
Pred. No. 3.1e-27;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 RRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Hono sapiens lactoferrin (HLF) mRNA.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: AY165046; AAN63998.1;
EMBL: AY178998; AAN75578.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Analysis.";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases
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LACTOTRANSFERRIN.
547BFC42C9267E67 CRC64;
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Last annotation update)
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Last sequence update)
Last annotation update)
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Lactotransferrin precursor (Lactoferrin).
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01-MAR-2003 (TrEMBLrel. 23, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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711 LA
78382 MW;
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Best Local Similarity 95./%;
Thes 45, Conservative
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| Similarity 95.7%;
| 45; Conservative
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactotransferrin.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             711 AA;
                                                                           SEQUENCE FROM N.A.
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Matches 4
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Q8IU92
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Gaps

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STRAIN-C57BL,63; TISSUB-Bone;
MEDLINE-2234683; PubMed=12466851;
The FANTOM Consortium.
The FANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
The FANTOM Consortium of the mouse transcriptome based on functional annotation of 60,770 full-length conner.

Mature 420:563-573(2002).

EMBL: AK036491; BAC29450.1; -.

EMBL: AK036491; BAC29450.1; -.
                                                                                                                                                                                                                                                                                                                                   Gaps
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0
                                                                                                                                                                                                                                                                   5 SVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA 48
                                                                                                                                                                                                                                                                                                                                                                                                      23 TVQWCAVSNSEEEKCLRWQNEMRKVGGPPLSCVKKSSTRQCIQA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Lactoferrin homolog (Fragment).
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SEQUENCE
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Wang S.-R., Lin T.-Y., Weng C.-N.;
Wang S.-R., Lin T.-Y., Weng C.-N.;
Wang S.-R., Lin T.-Y., Weng C.-N.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                          Sato I.; "Characterization of the 84-kDa protein with ABH activity in human
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                       sus sciona (rig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5,
                                                                                                                                                                                     Score 144.5; DB 4; Length 38; Pred. No. 4.3e-13; O; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 RRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Indels
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                                                                                                                                                            0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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; Pred. No. 2.3e-08;
10; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                               704 AA
                                                                                                             49:281-293(1995).
                                                                                                                                                                                                                                                                                                                                                        Created)
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01-MAY-2000 (TrEMBLrel. 13, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L77887; AAL40161.1;
InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR_FER; 2.
                                                                                                                                 InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 04021
                                               SEQUENCE FROM N.A.
MEDLINE-96081613; PubMed-8551695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        704. AA; 77681 MW;
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nilarity 81.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                      20,
20,
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Best Local Similarity 43.5%
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                         Lactoferrin (Fragment).
                                                                                                 seminal plasma.";
Jpn. J. Legal Med.
HSSP; 077811; 1B1X.
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nes 31; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                   scrofa (P1g).
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01-MAR-2002 (
01-OCT-2002 (
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Matches
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Q9TR80
ID Q9TR
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STRAIN-C57BL/64; TISSUB-Liver;

KAWAI J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

KAWAI J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

KAWAI T., Hara A., Fukunlah Y., Konno H., Adachi J., Fukuda S.,

A Azawa T., Atana M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Azawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Ragner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bash G.,

Brownstein M.J., Bulf C., Fletcher C., Fujita M., Garlincid B.,

Gustincich S., Hill D., Hofman M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

K. Sataki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-

K. Bulle Boris R., Wang K.H., Weltz C., Whittaker C., Wilming L.,

Myshaw-Boris A. Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                          Ovis aries (Sheep).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR0011156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                                                                                                                                                                                                                                         D., Fiat A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) Lactoferrin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 115; DB 6;
Pred. No. 5.3e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |::|:|||:|||3 RKNVRWCAISPPEGSKCYQWQKKMRKLGRP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 RRSVQWCAVSQPEATKCFQWQRNMRKVRGP 32
                                                                                                                                                                                                                                                                                                                                                   Odan Z.Y., Jolles P., Migliore-Samour D.
Biochim. Blophys. Acta 1243:25-32(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                    MEDLINE-95127729; PubMed-7827104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AK005035; BAB23762.1; -.
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PRINTS; PR00422; TRANSFERRIN.
SWART; SM00094; TR_FER; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.1%;
56.7%;
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17,
22,
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Best Local Similarity 56.7'
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 01-OCT-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; 077698; 1CE2
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SEQUENCE
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            DTT BE SEED BY SEED BY
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RA Tange N., Jong-Young L., Mikawa N., Hirono I., Aoki T.;
Tange N., Jong-Young L., Mikawa N., Hirono I., Aoki T.;
Tange N., Jong-Young L., Mikawa N., Hirono I., Aoki T.;
Tange N., Jong-Young L., Mikawa N., Hirono I., Aoki T.;
Tange N., Jong-Young L., Mikawa N., Hirono I., Aoki T.;
Tange N., Jong-Young L., Mikawa N., Hirono I., Aoki T.;
Tange N., Jong-Young L., Mikawa N., Hirono I., Aoki T.;
Tange N., Jong-Young L., Mikawa N., Hirono I., Aoki T.;
Tange N., Jong-Young L., Mikawa N., Hirono I., Aoki T.;
Tange N., Jong-Young L., Mikawa N., Hirono I., Aoki T.;
Tange N., Jong-Young L., Hirono I., Aoki T.;
Tange N., Jong-Young L., Hirono I., Aoki T., 
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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                           Aldred A.R., Howlett G.J., Schreiber G.; "Synthesis of rat transferrin in Escherichia coli containing recombinant bacteriophage.";
                                                                                                                                                                                                                                                                                                                                                                            Match 34.6%; Score 92.5; DB 11; Length 87; Local Similarity 41.5%; Pred. No. 2.1e-05; es 17; Conservative 11; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 RSVQWCAVSQPEATKCFQWQRNMRKV---RGPPVSCIKRDS 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 KTVXWCAVSEHENTKCISFRDHMKTVLPADGPRLACVKKTS 57
                                                                                                                                                                                                                                                                                                                           87 AA; 9487 MW; 1982C1D3FDDD3BA2 CRC64;
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Last annotation update)
                                                                                                              691 AA
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01-MAR-2002 (TrEMBLrel. 20, Created)
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MEDLINE-84307580; PubMed-6236811;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Q8UUK7
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MEDLINE-99363267; PubMed-10434423;
Ford M.J., Thornton P.J., Park L.K.;
"Natural selection promotes divergence of transferrin among salmonid
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                                                                                            Oncorhynchus kisutch (Coho salmon).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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  Last sequence update)
Last annotation update)
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1; JOINED.
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AAF03083.1; JOINED.
AAF03083.1; JOINED.
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PROSITE; PS00206; TRANSFERRIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                   MÖl. ECOl. 8:1055-1061(1999).
EMBL; AF114866; AAF03083.1; -
EMBL; AF114855; AAF03083.1; JOINED
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AAF03083.1; JOINED
AAF03083.1; JOINED
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SMART; SM00094; TR_FER; 2.
(TrEMBLrel. 20, (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00405; transferrin;
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hes 18; Conservative
                                                  Transferrin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           517 AA;
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                   NCBI_TaxID-8019;
                       I-OCT-2002
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Creation date: 12-31-2003

Indexing Officer: ANKIPIGI - ALLISON NKPIGI

Team: OIPEScanning Dossier: 09508095

Legal Date: 08-12-2003

No.	Doccode	Number of pages
1	CTNF	13
2	892	1
3	FOR	43

Total number of <sub>I</sub>	pages:	57
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Order of re-scan issued on .....